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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:09:40 : Search time 1534 Seconds  
(without alignments) 8651.160 Million cell updates/sec

Title: US-09-941-042C-1

Perfect score: 456

Sequence: 1 ggaacataatcaatacatt.....ggttaaaagagcttacagag 456

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

GenEmbl:\*

- 1: gb\_ba:\*\*
- 2: gb\_hvg:\*\*
- 3: gb\_in:\*\*
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- 5: gb\_ov:\*\*
- 6: gb\_pat:\*\*
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- 25: em\_pl:\*\*
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- 27: em\_sts:\*\*
- 28: em\_un:\*\*
- 29: em\_vl:\*\*
- 30: em\_htg\_hum:\*\*
- 31: em\_htg\_inv:\*\*
- 32: em\_htg\_other:\*\*
- 33: em\_htg\_mus:\*\*
- 34: em\_htg\_pln:\*\*
- 35: em\_htg\_rtd:\*\*
- 36: em\_htg\_man:\*\*
- 37: em\_htg\_vrt:\*\*
- 38: em\_sy:\*\*
- 39: em\_htgo\_hum:\*\*
- 40: em\_htgo\_mus:\*\*
- 41: em\_htgo\_other:\*\*

Pred. No. 18 the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	100.0	456	AX467562	AX467562 Sequence
2	456	100.0	1030	AR059251	AR059251 Sequence
3	456	100.0	1294	AR059250	AR059250 Sequence
4	456	100.0	1372	AR059249	AR059249 Sequence
5	456	100.0	1988	AR059248	AR059248 Sequence
6	456	100.0	2010	AR059247	AR059247 Sequence
7	245	53.7	2347	TOPBPAB	DA2070 Tobacco psa
8	184.2	40.4	6053	NT85A	X70902 N. Tobaccum T
9	148	32.5	722	AR059252	AR059252 Sequence
10	94.4	20.7	5040	NSCHRIB	X57079 N. sylvestri
11	69	15.1	157373	AL593856	AL593856 Human DNA
12	68.8	15.1	116696	PMAL3P3	Z98547 Plasmodium
13	66.8	14.6	150199	AC087568	AC087568 Pan trogl
14	66.6	14.6	5145	AX281353	AX281353 Sequence
15	66.6	14.6	5145	AX345250	AX345250 Sequence
16	66.4	14.6	8305	AX346470	AX346470 Sequence
17	65.6	14.4	149497	AL627305	AL627305 Dantio rer
18	65.4	14.3	3945	AF141654	AF141654 Nicotiana
19	65.2	14.3	234112	PMAL4P2	AL035475 Plasmodiu
20	65	14.3	152797	AC108052	AC108052 Homo sapi
21	64.8	14.2	194943	AC105252	AC105252 Homo sapi
22	64.6	14.2	44067	AC011463	AC011463 Homo sapi
23	64.6	14.2	101944	AL357136	AL357136 Human DNA
24	64.2	14.1	155106	AC104069	AC104069 Homo sapi
25	63.8	14.0	195130	AL359832	AL359832 Human DNA
26	63.2	13.9	135711	VT1VD10	AL360354 Plasmodiu
27	63	13.8	124820	AC117073	AC117073 Dictyoste
28	63	13.8	158813	AC080091	AC080091 Homo sapi
29	62.8	13.8	91798	HSKB152G3	AL132982 Human DNA
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32	62.6	13.7	169541	AL136178	AL136178 Human DNA
33	62.4	13.7	38013	AL590287	AL590287 Human DNA
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35	62.4	13.7	176368	CNS01RGG	AL157971 Human chr
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43	62	13.6	198853	AL365354	AL365354 Homo sapi
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ALIGNMENTS

RESULT 1  
AX467562  
LOCUS AX467562 456 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 1 from Patent WO0218607.  
ACCESSION AX467562  
VERSION AX467562.1 GI:21900757  
KEYWORDS  
SOURCE  
ORGANISM Common tobacco.  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Nicotiana.  
REFERENCE  
AUTHORS Conkling, M.A. and Li, Y.  
TITLE Transgenic plants containing molecular decoys that alter protein

Journal content therein  
 Patent: WO 0218607-A 1 07-MAR-2002;  
 NORTH CAROLINA STATE UNIVERSITY (US)  
 Location/Qualifiers  
 source 1..456  
 /organism="Nicotiana tabacum"  
 /db\_xref="taxon:4097"

BASE COUNT 158 a 57 c 66 g 175 t  
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 Pred. No. 2.6e-59; Mismatches 0; Gaps 0;  
 Matches 456; Conservative 0; Indels 0;

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 DB 421 CCTAGTTGTTGTTATAGATTTATTAATAAATTCAGGTTCTTACAGAG 456

RESULT 2  
 LOCUS AR059251 1030 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 5 from patent US 5837876.  
 ACCESSION AR059251  
 VERSION AR059251.1 GI:5984828  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1030)  
 AUTHORS Conkling M.A., Mendu N. and Song W.  
 TITLE Root cortex specific gene promoter  
 JOURNAL Patent: US 5837876-A 5 17-NOV-1998;  
 FEATURES  
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 /organism="unknown"

BASE COUNT 388 a 143 c 164 g 335 t  
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 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 AATTAATCGGTACAGTTATAGATTTATTAATAAATTCAGGTTCTTACAGAG 456  
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 QY 241 TTTAATCGGTACAGTTATAGATTTATTAATAAATTCAGGTTCTTACAGAG 456  
 DB 241 TTTAATCGGTACAGTTATAGATTTATTAATAAATTCAGGTTCTTACAGAG 456  
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BASE COUNT 515 a 174 c 203 g 402 t  
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 Best Local Similarity 100.0%; Pred. No. 2e-59;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 361 AATCGGTTCCGGTCCGAGCGGTTCCGATTCGATTTTCAATTTTATTAATAAATTCAGGTTCTTACAGAG 456  
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RESULT 3  
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 DEFINITION Sequence 4 from patent US 5837876.  
 ACCESSION AR059250  
 VERSION AR059250.1 GI:5984827  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1294)  
 AUTHORS Conkling M.A., Mendu N. and Song W.  
 TITLE Root cortex specific gene promoter  
 JOURNAL Patent: US 5837876-A 4 17-NOV-1998;  
 FEATURES  
 source Location/Qualifiers  
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 /organism="unknown"

BASE COUNT 515 a 174 c 203 g 402 t  
 ORIGIN

Query Match 100.0%; Score 456; DB 6; Length 1294;  
 Best Local Similarity 100.0%; Pred. No. 2e-59;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAAACATATTCANATTCATTTGAGTTGGCTACTCAATTCGCTAGAAATCTTTGTCCTT 60  
 |||

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OK nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:09:40 ; Search time 1534 Seconds

(Without alignments) 8651.160 Million cell updates/sec

Title: US-09-941-042C-1

Perfect score: 456  
Sequence: 1 ggaacatcatcatcatc.....gtaaaagaggtacagag 456

Scoring table: IDENTITY NDC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: gb\_da:\*\*
- 2: gb\_hlg:\*\*
- 3: gb\_in:\*\*
- 4: gb\_om:\*\*
- 5: gb\_ov:\*\*
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- 33: em\_htg\_mus:\*\*
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- 37: em\_htg\_vrt:\*\*
- 38: em\_htg:\*\*
- 39: em\_htgo\_hum:\*\*
- 40: em\_htgo\_mus:\*\*
- 41: em\_htgo\_other:\*\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	100.0	456	AX467562	AX467562 Sequence
2	456	100.0	1030	AR059251	AR059251 Sequence
3	456	100.0	1294	AR059250	AR059250 Sequence
4	456	100.0	1372	AR059249	AR059249 Sequence
5	456	100.0	1988	AR059248	AR059248 Sequence
6	456	100.0	2010	AR059247	AR059247 Sequence
7	245	53.7	2347	TOBPSAEB	TOBPSAEB
8	184.2	40.4	6053	NTT85A	NTT85A
9	148	32.5	722	AR059252	AR059252 Sequence
10	94.4	20.7	5040	NSCHRIB	NSCHRIB
11	69	15.1	157373	AL593856	AL593856 Human DNA
12	68.8	15.1	116696	PEMAL3P3	PEMAL3P3 Plasmidium
13	66.8	14.6	150199	AC087568	AC087568 Pan trog1
14	66.6	14.6	5145	AX281353	AX281353 Sequence
15	66.6	14.6	5145	AX345250	AX345250 Sequence
16	66.4	14.6	8305	AX345470	AX345470 Sequence
17	65.6	14.4	149497	AL627305	AL627305 Dantio Ter
18	65.4	14.3	3945	AF141654	AF141654 Nicotiana
19	65.2	14.3	234112	PEMAL4P2	PEMAL4P2 Plasmidium
20	65	14.3	152797	AC108052	AC108052 Homo sapi
21	65	14.3	194943	AC105252	AC105252 Homo sapi
22	64.8	14.2	101944	AC011463	AC011463 Homo sapi
23	64.6	14.2	44067	AL357136	AL357136 Human DNA
24	64.2	14.1	155106	AC104069	AC104069 Homo sapi
25	63.8	14.0	195130	AL359832	AL359832 Human DNA
26	63.2	13.9	155711	VIYVD10	VIYVD10 Dictyoste
27	63	13.8	124820	AC117073	AC117073 Dictyoste
28	63	13.8	158813	AC080091	AC080091 Homo sapi
29	62.8	13.8	91798	HSKB152G3	HSKB152G3 Human DNA
30	62.8	13.8	96953	AC079621	AC079621 Homo sapi
31	62.6	13.7	145598	AC008132	AC008132 Homo sapi
32	62.6	13.7	169541	AL136178	AL136178 Human DNA
33	62.4	13.7	38013	AL590287	AL590287 Human DNA
34	62.4	13.7	110000	PEMAL4P1_1	PEMAL4P1_1 ContInuaction (2 of
35	62.4	13.7	176368	CNS01RG6	AL157971 Human chr
36	62.2	13.6	103344	HS1100E15	AL035551 Human DNA
37	62.2	13.6	165260	AC024341	AC024341 Homo sapi
38	62.2	13.6	165423	CNS07BCV	AL442653 Human chr
39	62.2	13.6	224448	PEMAL4P4	AL035477 Plasmidiu
40	62	13.6	1266	DDI301668	AJ010568 Dictyoste
41	62	13.6	1792	AF151388	AF151388 Dermalobi
42	62	13.6	186431	AC022281	AC022281 Homo sapi
43	62	13.6	198853	AL365354	AL365354 Homo sapi
44	61.8	13.6	106090	AL732577	AL732577 Zebrafish
45	61.8	13.6	167362	AC006269	AC006269 Homo sapi

ALIGNMENTS

RESULT 1  
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 DEFINITION Sequence 1 from Patent WO0218607.  
 ACCESSION AX467562  
 VERSION AX467562.1 GI:21900757  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Common tobacco.  
 Nicotiana tabacum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Pred. No. is the number of results predicted by chance to have a

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QY 301 AATTAATCGGTACAGTATTAAGATTTTATAAATAAATTAATTAATTAACCTTACCCCT 560

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QY 421 CCTAGTTGTTGTTATTAAGTAAATAAAGCAGTTACAGAG 456

Db 685 CCTAGTTGTTGTTATTAAGTAAATAAAGCAGTTACAGAG 720

RESULT 4  
AR059249 1372 bp DNA linear PAR 29-SEP-1999  
LOCUS AR059249 Sequence 3 from patent US 5837876.  
DEFINITION AR059249  
ACCESSION AR059249  
VERSION AR059249.1 GI:5984826  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1372)  
AUTHORS ConKling,M.A., Mendu,N. and Song,M.  
TITLE Root cortex specific gene promoter  
JOURNAL Patent: US 5837876-A 3 17-NOV-1998;  
FEATUERS Location/Qualifiers  
1..1372

BASE COUNT 532 a 187 c 215 g 438 t  
ORIGIN

Query Match 100.0%; Score 456; DB 6; Length 1372;  
Best Local Similarity 100.0%; Pred. No. 1,9e-59;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 343 GGAAACATATTAATTAAGTTCATTTGTTTAAATTAATTAATTAACCTTACCCCT 402

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QY 181 ATGAAAATTTTAAATGCTTATTAAGTTCATTAATTAATTAATTAATTAACCTTACCCCT 240

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Db 643 AATTAATCGGTACAGTATTAAGATTTTATAAATAAATTAATTAATTAACCTTACCCCT 702

QY 361 AATTCGGTTGCGGCGGACGGTTCGATCGGTTAGTTCGATTTTCAAAATTTTCAATTCAGCACT 420

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QY 421 CCTAGTTGTTGTTATTAAGTAAATAAAGCAGTTACAGAG 456

Db 763 CCTAGTTGTTGTTATTAAGTAAATAAAGCAGTTACAGAG 798

RESULT 5

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LOCUS AR059248 Sequence 2 from patent US 5837876.  
DEFINITION AR059248  
ACCESSION AR059248  
VERSION AR059248.1 GI:5984825  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1988)  
AUTHORS ConKling,M.A., Mendu,N. and Song,M.  
TITLE Root cortex specific gene promoter  
JOURNAL Patent: US 5837876-A 2 17-NOV-1998;  
FEATUERS Location/Qualifiers  
1..1988

BASE COUNT 714 a 271 c 302 g 701 t  
ORIGIN

Query Match 100.0%; Score 456; DB 6; Length 1988;  
Best Local Similarity 100.0%; Pred. No. 1.7e-59;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAACATATTAATTAAGTTCATTTGTTTAAATTAATTAATTAACCTTACCCCT 60

Db 959 GGAAACATATTAATTAAGTTCATTTGTTTAAATTAATTAATTAACCTTACCCCT 1018

QY 61 GCTAAATGATAGTACAGTTCATTAATTAATTAATTAATTAATTAACCTTACCCCT 120

Db 1019 GCTAAATGATAGTACAGTTCATTAATTAATTAATTAATTAATTAACCTTACCCCT 1078

QY 121 ATTAGTATTTTGAAGTTCATTAATTAATTAATTAATTAATTAACCTTACCCCT 180

Db 1079 ATTAGTATTTTGAAGTTCATTAATTAATTAATTAATTAATTAACCTTACCCCT 1138

QY 181 ATGAAAATTTTAAATGCTTATTAAGTTCATTAATTAATTAATTAATTAACCTTACCCCT 240

Db 1139 ATGAAAATTTTAAATGCTTATTAAGTTCATTAATTAATTAATTAATTAACCTTACCCCT 1198

QY 241 TTAAATCGGTATAGTTCATTAATTAATTAATTAATTAATTAACCTTACCCCT 300

Db 1199 TTAAATCGGTATAGTTCATTAATTAATTAATTAATTAATTAACCTTACCCCT 1258

QY 301 AATTAATCGGTACAGTATTAAGATTTTATAAATAAATTAATTAATTAACCTTACCCCT 360

Db 1259 AATTAATCGGTACAGTATTAAGATTTTATAAATAAATTAATTAATTAACCTTACCCCT 1318

QY 361 AATTCGGTTGCGGCGGACGGTTCGATCGGTTAGTTCGATTTTCAAAATTTTCAATTCAGCACT 420

Db 1319 AATTCGGTTGCGGCGGACGGTTCGATCGGTTAGTTCGATTTTCAAAATTTTCAATTCAGCACT 1378

QY 421 CCTAGTTGTTGTTATTAAGTAAATAAAGCAGTTACAGAG 456

Db 1379 CCTAGTTGTTGTTATTAAGTAAATAAAGCAGTTACAGAG 1414

RESULT 6  
AR059247 2010 bp DNA linear PAR 29-SEP-1999  
LOCUS AR059247 Sequence 1 from patent US 5837876.  
DEFINITION AR059247  
ACCESSION AR059247  
VERSION AR059247.1 GI:5984824  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2010)  
AUTHORS ConKling,M.A., Mendu,N. and Song,M.  
TITLE Root cortex specific gene promoter  
JOURNAL Patent: US 5837876-A 1 17-NOV-1998;  
FEATUERS Location/Qualifiers  
1..2010









/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="1"  
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 /clone\_1kb="RPC1-11.1"  
 21893..22113  
 /note="Sequence from overlapping clone RP11-49P4 (AL136373). Assembly confirmed by restriction digest."  
 133321..132460  
 /note="Sequence from overlapping clone RP4-723G19 (AL356793). Assembly confirmed by restriction digest."  
 misc\_feature  
 BASE COUNT 45193 a 32904 c 32733 g 46543 t  
 ORIGIN  
 Query Match 15.1%; Score 69; DB 9; Length 157373;  
 Best local similarity 54.3%; Pred. No. 0.037;  
 Matches 183; Conservative 0; Mismatches 150; Indels 4; Gaps 2;  
 QY 5 ACATATTCACATGACAGTTGAGTTCGATGCAATGCGCTAGAAATCCTTGTGCCTGCCTA 64  
 DB 130171 ATATATTTTAAATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 130112  
 QY 65 ATTAAGTACTGTGAAAGCTTAAATTAATAATGAAATGCAATGATTAATATGAGATTTAGCAATT 123  
 DB 130111 ATATATTTTAAATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 130052  
 QY 124 AGATATTTGAGTTAAATTAATCTTATGACCTGTAACAGTGTATTTAAATTCGAAGCCGATG 183  
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 QY 184 AAAAATTTAATGCTTTAATGATTTAATGATTTAATGATTTAATGATTTAATGATTTAATGAT 240  
 DB 129991 ATAAATTTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 129932  
 QY 241 TTTAAATCGGTAAATGATTTGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 300  
 DB 129931 TATAATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 129872  
 QY 301 AATTAATCGGTAAATGATTTAATGATTTAATGATTTAATGATTTAATGATTTAATGATTT 337  
 DB 129871 ATATATTTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 129835  
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 PFMAL3P3/c 116696 bp DNA linear INV 27-APR-2000  
 LOCUS PFMAL3P3 116696 bp complete sequence.  
 DEFINITION Plasmodium falciparum MAL3P3, complete sequence.  
 ACCESSION Z98547 AL008977 AL010164 AL139179 Z98548 Z98549 Z98550  
 VERSION Z98547.2 GI:15383894  
 KEYWORDS HMG; 60S Acidic ribosomal protein P2; asparagine synthetase; calcium-dependent protein kinase; DNA polymerase delta; dual specificity protein phosphatase; guanine nucleotide-binding protein kinases; T-complex protein eta; TORB1.2-1-like protein; WD domain; Y48E1C.2-1-like protein.  
 SOURCE Plasmodium falciparum 3D7.  
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 REFERENCE 1 (bases 1 to 116696)  
 AUTHORS Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,R., Felwell,T., Gentles,S., Gilliam,R., Hamlin,N., Harris,D., Holtroft,S., Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J., Mould,S., Mungall,K., Murphy,L., Olliver,K., Quail,M.A., Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S., Sulston,J.E., Whitehead,S., Woodward,J.R., Neohold,C. and Barrett,B.G.  
 TITLE The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum  
 JOURNAL Nature 400 (6744), 532-538 (1999)  
 MEDLINE 93376085  
 PUBMED 10448855  
 REFERENCE 2 (bases 1 to 116696)

AUTHORS Mungall,K., Bowman,S., Churcher,C., Lawson,D., Quail,M., Rajandream,M.-A. and Barrett,B.  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 116696)  
 AUTHORS Lawson,D., Bowman,S. and Barrett,B.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-AUG-1997) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK  
 COMMENT On or before Aug 31, 2001 this sequence version replaced g1:2894463, g1:2894495, g1:2894569, g1:2982521, g1:2665376, g1:3649752.  
 For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P\_falciparum. The following numbers may have changed slightly:  
 The true left end of clone MY549-3D7 is at 1 in this sequence. The true right end of clone MY434-3D7 is at 114736 in this sequence.  
 Location/Qualifiers  
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 /strain="3D7"  
 /db\_xref="taxon:36329"  
 /chromosome="3"  
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 /note="exon 2 of PFC0235c"  
 complement(4804..4830)  
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 gene  
 complement(4740..4839)  
 /gene="PFC0330w, MAL3P3.2"  
 6740..8839  
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 6740..8839  
 /note="PFC0330w (MAL3P3.2), putative PDZ domain protein, len: 700 aa, Match to PFC00595 PDZ, PDZ domain (Also known as DHR or GLGF). Score 20.36, predicted using hexexon  
 /codon\_start=1  
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 /db\_xref="GI:3649753"  
 /db\_xref="SP:PREMBL:077318"  
 /translation="MYLLMSKFLVWIIIFGNFVYHFPLFKIPNNKITVLFYDNSK KORINSHNFFLYKNDFLNLKLNKRRKHLFVYRKKKEDIOESGYLYPFDHLEKKK KFPDPYIIPSEDEKESIDIPEHKINDDDMIYRDDDAKRYRKPETPKRNIIOKDE NSEDDQDDLDNDQDDINNFTNNTLNTPNPNSTNPNNSIDNPNNNSIDNPNNNSI DNPNNNSIDNPNNNSIDNPNNNSIDNPNNNSIDNPNNNSIDNPNNNSIDNPNNNSI KTDIEKDIININEFYSSESEKTIACEMIQDQYLHLSDDKFKFTFNINIESHVPSE KRICVSYNMSKHPFRSISINSDLIERSNKLYVLERIHHLYEDDKNENAYAKKTL PKEYIEGKRERDYNLKSNNKMSIESSLKIEKCMQNRKONVEITLHDKLVNML RKKYRFFLSLWCTSTISLTYVNDLQGFRTFAKKSITYEKKYVAVAKCGDAVRSR KFWAKNFYDIAITLGRKDEGERFEDIVQELNMTERRAKLVDLKEHNRNSRIITL KNNIGYLVNKNPDSIGGYVYSIIEGSVASAKNLHGGQVIALNNHVTYGGPFDQCLK AFQKNDGTQYDIIFFPKGINIELYGLKAVYIKRNDLJFALFENQIVSEKRNETILFDM KGFSTFSEYSGMSKRAEPV"  
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 /note="Match to PFC00595 PDZ, PDZ domain (Also known as DHR or GLGF). Score 20.36  
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 /gene="PFC0335c, MAL3P3.3", hypothetical protein, len: 3724 aa, predicted using hexexon"  
 /codon\_start=1



TITLE  
 JOURNAL McCluskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,  
 Stantipopol, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,  
 Tsurgren, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Zhang, L.-H. and Green, E.D.  
 NISC Comparative Sequencing Initiative  
 Unpublished  
 2 (bases 1 to 150199)

REFERENCE  
 AUTHORS Direct Submission  
 JOURNAL Submitted (10-JUN-2001) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 3 (bases 1 to 150199)  
 Green, E.D.  
 REFERENCE Direct Submission  
 AUTHORS Submitted (02-NOV-2001) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 On Nov 2, 2001 this sequence version replaced gi:12061434.

COMMENT

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc.mouse@hghl.nih.gov  
 ----- Project Information  
 Center project name: a01  
 Center clone name: 135M11

This sequence was finished as follows unless otherwise noted:  
 all regions were double-stranded, sequenced with an  
 alternate chemistry, or covered by high quality data  
 (i.e., phred quality >= 30); an attempt was made to resolve  
 all sequencing problems, such as compressions and repeats;  
 all regions were covered by at least one plasmid subclone  
 or more than one M13 subclone; and the assembly was confirmed  
 by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of  
 this clone unless otherwise noted. If there are overlapping  
 clones, the overlaps are noted in the beginning and end of  
 the features section.

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 /db\_xref="taxon:9598"  
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 BASE COUNT 36501 a 36322 c 37037 g 40339 t  
 ORIGIN

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 Best Local Similarity 48.7%: Pred. No. 0.08;  
 Matches 182; Conservative 0; Mismatches 192; Indels 0; Gaps 0;  
 QY 73 ACTTGAATAGCTTAAATATTAATTAATAGCATATGAGATTTGATTTGG 132  
 DB 38689 ACTATATAGCTTTATATATTAATTAATTAATGATTTGATTTGG 132  
 QY 133 AGTTAAATTTACTTATTTGGCTTGAACAGTTTTAAATTTTCCAGGCCCCAAGAAATTA 192  
 DB 38748 AGTTAAATTTACTTATTTGGCTTGAACAGTTTTAAATTTTCCAGGCCCCAAGAAATTA 192  
 QY 38749 ATATTTATAAACCATATATATATATATATATATATATATAATAT 38808  
 DB 193 ATGCCTTATTAGTTTAACAATACTACTATATATATATATATATATAT 252  
 QY 38809 ATTTTATATTTTATATATATATATATATATATATATATATATATATAA 38868  
 DB 253 AGTTGGATATTTTTCATTTATTTATTTATAATTAATTAATTAATTAAT 312  
 QY 38869 ATATATAATATATATTTATTTTATATATATATATATATATATAT 38928  
 DB 313 AGTTTATATTTATATATATATATATATATATATATATATATATATA 372  
 QY 38929 TAATATAAACAATAATATATATATATATATATATATATATATATA 38988  
 QY 373 GCGGACGGTTCATGATTTTGTGTGATTTTGAACACATTCATTTGACACT 432

Db 38989 TAATATAAACAATAATATATATATATATATATATATATATATA 39048  
 QY 433 TATAGCTAAAAAGC 446  
 Db 39049 TATATTAATTAATAAC 39062

RESULT 14

AX281353 5145 bp DNA linear PAT 02-NOV-2001  
 LOCUS Sequence 17 from Patent W00177376.  
 DEFINITION AX281353  
 ACCESSION AX281353  
 VERSION AX281353.1 GI:16608608

SYNTHETIC CONSTRUCT.  
 ARTIFICIAL SEQUENCES.  
 SOURCE synthetic construct.  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.  
 TITLE Diagnosis of diseases associated with metastasis  
 JOURNAL Patent: WO 0177376-A 17 18-OCT-2001;  
 Epigenomics AG (DE)

FEATURES  
 source Location/Qualifiers  
 1..5145  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="chemically treated genomic DNA (Homo sapiens)"

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 Best Local Similarity 51.9%: Pred. No. 0.22;  
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QY 4 AACATATTCAAATACATTTGTTTCTCCTAATAATGCTTGAATTTGCTCTCT 63  
 DB 511 AATATATTTTAAAGTTTAAAGTTTAAATATTTTGGGTATATTTTGGGTTT 570  
 QY 64 AATAAAGTACTTGAATTAAGTTTAAATATATTAATTAATTAATTAATTA 123  
 DB 571 TATGTTTAAAGGGCTATATATATTTTAATTTAAAGTGTTTTTTTTTTT 630  
 QY 124 AGTATTTGAGTATTAATTTACTTTATTTGACTTTGACAGTTTTATTAATTT 183  
 DB 631 TTTTTTTTTAGTTTGTTTATTAAGGTTTTTTAGTTTACGAATTAAGATAA 686  
 QY 184 AAAAAATTAATGCTTATTTACTTTTAACTTATTAATTAATTTTAAATTT 243  
 DB 687 AAAAAATTAATTTTATTTTATTTTATTTTAAATTTGATTTGTTTTTTA 746  
 QY 244 AATGCTTAAAGTCTTAAATTTTTCATTTTAAATTTTAAATTAATTAAT 303  
 DB 747 TGTATATTTTATGATTTTATTAATTAATTTTAAATTTTAAATTTTAA 806  
 QY 304 TATGCTTAAAGTCTTAAATTTTTCATTTTAAATTTTAAATTTTAAAT 342  
 DB 807 TTTTCTTTTAAATTTGATTTTATTAATTAATTTTAAATTTTAAATTTA 845

RESULT 15  
 AX345250 5145 bp DNA linear PAT 01-FEB-2002  
 LOCUS Sequence 321 from Patent W00200928.  
 DEFINITION AX345250  
 ACCESSION AX345250  
 VERSION AX345250.1 GI:18493136  
 KEYWORDS synthetic construct.  
 SOURCE synthetic construct.  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.  
 TITLE Diagnosis of diseases associated with the immune system

JOURNAL Patent: WO 0200928-A 321 03-JAN-2002;

Epigenomics AG (DE)

FEATURES Location/Qualifiers

1. 5145 /organism="synthetic construct"

/db\_xref="taxon:32630" /note="chemically treated genomic DNA (Homo sapiens)"

BASE COUNT 1470 a 27 c 855 g 2793 t

ORIGIN

Query Match 14.6%; Score 66.6; DB 6; Length 5145;

Best Local Similarity 51.9%; Pred. No. 0.22;

Matches 176; Conservative 0; Mismatches 159; Indels 4; Gaps 1;

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DB 511 AATATATTTTAAAGTTAAAGTTAAATATTTTGGGTATTTATTTATTTGGGTGTTT 570
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OY 64 AATAAAGTACTTGAATAAGCTTAGTTAAATATTAATAGCATATATAGATTTAGCAAT 123
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DB 571 TATGTTATGAGGGATATATATTTAATTAATGATGTTTTTTTTTTTAAATTTG 630
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OY 124 AGTATTTGAGTTAATTTACTTATTGACTGTACAGTTTTTAAATTCAGGCCCATG 183
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DB 631 TTTTTTTTACTTTGGTTTATAGGGTTTTAGTTAGAGATTTAAGATTAAGAAG---AGG 686
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OY 184 AAAAATTTAATGCTTATTTAGTTTAACTTACTTATTAATTTTTCATTTGTAATAATTT 243
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DB 687 AAAAAGATTAATTTTATTTTAAATTTGGGATTTGTTTATATTTTATTTAGTT 746
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OY 244 AATCGTATAGTTCGATATTTTTCATTTTATTTTAAATTAATAAATAAATACCTTAA 303
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DB 747 TGTATATTTATGATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTAA 806
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OY 304 TATCGTACAGTTATAGATTTAATTAATAAATCTACGGTT 342
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DB 807 TTTTGTTTTAAATATTTGATATATTAATAATTTATAGTT 845
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Job time : 1538 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:08:40 ; Search time 190 Seconds  
(Without alignments)  
5404.796 Million cell updates/sec

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Perfect score: 456  
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues  
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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
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  - 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	456	100.0	456	24	ABL58286
2	456	100.0	1030	18	AAAT51750
3	456	100.0	1294	18	AAAT51749
4	456	100.0	1372	18	AAAT51748
5	456	100.0	1988	18	AAAT51747
6	451.2	98.9	2010	18	AAAT51746
7	148	32.5	722	18	AAAT51751
8	66.6	14.6	5145	24	ABL332348
9	66.6	14.6	5145	24	ABL344464

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C 11	61	13.4	6175	24	ABL33307
C 12	60.4	13.2	18997	24	ABL33948
C 13	60.4	13.2	18997	24	ABL32570
C 14	60.2	13.2	5925	24	ABL33576
C 15	60	13.2	8305	24	ABL33565
C 16	60	13.2	20420	22	AAK73165
C 17	60	13.2	20420	24	ABK69933
C 18	59.6	13.1	5407	24	ABL34091
C 19	59.4	13.0	20674	21	AAC58017
C 20	59	12.9	494	23	ABV10021
C 21	58.2	12.8	422	22	AAI15924
C 22	58.2	12.8	700	22	AAH93026
C 23	58.2	12.8	8842	24	ABL33449
C 24	58.2	12.8	8842	24	AA563335
C 25	58	12.7	6062	24	AA561094
C 26	58	12.7	8197	24	ABL70542
C 27	58	12.7	8197	24	ABL34515
C 28	57.6	12.6	6050	22	AA546792
C 29	57.6	12.6	6050	24	ABK33937
C 30	57.6	12.6	6050	24	ABL34129
C 31	57.6	12.6	10279	24	ABL92277
C 32	57.6	12.6	10279	24	ABL33591
C 33	57.6	12.6	10279	24	AAAD2328
C 34	57.2	12.5	8085	22	AA546479
C 35	57.2	12.5	8085	24	ABK33986
C 36	57	12.5	10886	24	ABL34135
C 37	57	12.5	16258	24	ABL70376
C 38	57	12.5	16258	24	ABK40038
C 39	56.8	12.5	3296	23	ABL17264
C 40	56.6	12.4	6013	24	AA561265
C 41	56.6	12.4	6013	24	AAK31361
C 42	56.6	12.4	6095	22	AA546310
C 43	56.6	12.4	6095	24	ABL70150
C 44	56.6	12.4	6095	24	ABL32361
C 45	56.6	12.4	6095	24	ABL34475

ALIGNMENTS

RESULT 1	ID	Score	Match	Query Length	DB ID	Description
ABL58286	ABL58286	standard;	DNA;	456	BP.	
ABL58286;	XX					
15-JUL-2002 (first entry)	DT					
N. tabacum Nic gene product responsive element DNA sequence.	DE					
Tobacco; plant; cis-acting element; transgenic; nicotine; Nic;	KW					
NCQPT1; nitrosamine; responsive element; ds.	KW					
Nicotiana tabacum.	OS					
MO200218607-A2.	PN					
07-MAR-2002.	PD					
28-AUG-2001; 2001WC-US26788.	PF					
30-AUG-2000; 2000US-229198P.	PR					
(UYNC-) UNIV NORTH CAROLINA STATE.	PA					
Conkling MA, LI Y;	PI					
WPI; 2002-371827/40.	DR					
Obtaining plant with altered levels of desired protein regulated	PT					
cis-acting element by introducing nucleic acid with the element not	PT					
operably linked to coding sequence of the protein to produce a	PT					

PR transformed cell  
XX  
PS Claim 1; Page 48; 48pp; English.

CC The invention provides a method of obtaining a plant with altered content  
CC of desired protein (P1) which is regulated by cis-acting element (E1).  
CC The method involves introducing exogenous nucleic acid (ENA) construct  
CC comprising E1 which is not operably linked to coding sequence or its  
CC complement of P1, into plant cell to produce transformed plant cell,  
CC where the cell contains ENA copies to alter level of P1 in plant  
CC regenerated from cells. The method is useful for obtaining a plant,  
CC preferably transgenic tobacco plant with altered content of P1,  
CC preferably a reduced amount of nicotine, which is regulated by E1 which  
CC is a Nic gene product, where altered content of P1 may be tobacco  
CC specific nitrosamines. The present sequence represents the N. tabacum  
CC Nic gene product responsive element DNA sequence.

XX Sequence 456 BP; 158 A; 57 C; 66 G; 175 T; 0 other:

Query Match 100.0%; Score 456; DB 24; Length 456;  
Best Local Similarity 100.0%; Pred. No. 4,3e-68;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 GGAAACATATTCATTAATTCAGTATTTGCTGCAATGCGTGCAGAAATATTGTTGGCTT 60  
DB 1 GGAAACATATTCATTAATTCAGTATTTGCTGCAATGCGTGCAGAAATATTGTTGGCTT 60  
YY 61 GCTAATAAAGATCTGGATAAAGCTTGTAAATATTAATAAGCATATTAATTTAGA 120  
DB 61 GCTAATAAAGATCTGGATAAAGCTTGTAAATATTAATAAGCATATTAATTTAGA 120  
YY 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
DB 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
YY 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
DB 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
YY 181 ATGAAAAATTTAATGCTTATTAAGTAAATCTACATAATTAATTTTCCATTATGTA 240  
DB 181 ATGAAAAATTTAATGCTTATTAAGTAAATCTACATAATTAATTTTCCATTATGTA 240  
YY 241 TTTAATGCGTAACTGATTTTCAATTTTATTTAATTTAATAAATAAAGCTTACCT 300  
DB 241 TTTAATGCGTAACTGATTTTCAATTTTATTTAATTTAATAAATAAAGCTTACCT 300  
YY 301 AATTATGCGTACAGTATTAAGTATTAATAATAAATCTACAGTTCACAGAAACCTTAA 360  
DB 301 AATTATGCGTACAGTATTAAGTATTAATAATAAATCTACAGTTCACAGAAACCTTAA 360  
YY 361 AATCGGTTCGGTGGGACGGTTCATCGGTTTACAGATTTTCAAAATATTCATTGACACT 420  
DB 361 AATCGGTTCGGTGGGACGGTTCATCGGTTTACAGATTTTCAAAATATTCATTGACACT 420  
YY 421 CCTAGTTGGTGTATTAAGTAAATAAGCAGTTTACAGAG 456  
DB 421 CCTAGTTGGTGTATTAAGTAAATAAGCAGTTTACAGAG 456  
RESULT 2  
AAT51750  
ID AAT51750 standard; DNA; 1030 BP.  
AC AAT51750;  
XX AAT51750;  
XX 15-Oct-1997 (first entry)  
XX  
XX Root cortex specific gene TobRD2 promoter (dell.0).  
KW Root cortex specific promoter; TobRD2; tobacco; transgenic plant;  
KW Insecticide; Bacillus thuringiensis; biological control; ss.  
XX Nicotiana tabacum.  
XX M09705261-A1.  
XX

PD 13-FEB-1997.  
XX  
XX 24-JUL-1996; 96W0-US12158.  
XX  
XX 28-JUL-1995; 95U5-0508786.  
XX  
XX (DYN-C-) UNIV NORTH CAROLINA STATE.  
XX  
XX Conkling MA, Mendu N, Song W;  
XX WPI: 1997-145698/13.  
XX

DR DNA directing heterologous gene expression in the root cortex - used  
PT e.g. for expressing insecticidal Bacillus proteins  
XX  
PS Claim 1; Page 37; 53pp; English.

XX An isolated DNA (AAT51750), designated dell.0, comprises a 1030 bp  
CC 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see  
CC also AAT51746), which directs root cortex-specific expression of  
CC associated genes. Dell.0 can be used in DNA cassettes to direct  
CC the expression of heterologous genes in the root cortex layer of  
CC transgenic monocot or dicot plants, e.g. Bacillus thuringiensis  
CC crystal proteins in tobacco for the control of root-damaging pests.  
CC Dell.0 conferred high levels of GUS reporter gene expression  
CC (several-fold higher than the CaMV35S promoter) in transgenic  
XX tobacco root cortex.

XX Sequence 1030 BP; 388 A; 143 C; 164 G; 335 T; 0 other:

Query Match 100.0%; Score 456; DB 18; Length 1030;  
Best Local Similarity 100.0%; Pred. No. 4e-68;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 GGAAACATATTCATTAATTCAGTATTTGCTGCAATGCGTGCAGAAATATTGTTGGCTT 60  
DB 1 GGAAACATATTCATTAATTCAGTATTTGCTGCAATGCGTGCAGAAATATTGTTGGCTT 60  
YY 61 GCTAATAAAGATCTGGATAAAGCTTGTAAATATTAATAAGCATATTAATTTAGA 120  
DB 61 GCTAATAAAGATCTGGATAAAGCTTGTAAATATTAATAAGCATATTAATTTAGA 120  
YY 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
DB 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
YY 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
DB 121 ATTAGTATTTGAGTAAATTAATTTGACTGTTAACAGATTTTAAATTCGAAGGCC 180  
YY 181 ATGAAAAATTTAATGCTTATTAAGTAAATCTACATAATTAATTTTCCATTATGTA 240  
DB 181 ATGAAAAATTTAATGCTTATTAAGTAAATCTACATAATTAATTTTCCATTATGTA 240  
YY 241 TTTAATGCGTAACTGATTTTCAATTTTATTTAATTTAATAAATAAAGCTTACCT 300  
DB 241 TTTAATGCGTAACTGATTTTCAATTTTATTTAATTTAATAAATAAAGCTTACCT 300  
YY 301 AATTATGCGTACAGTATTAAGTATTAATAATAAATCTACAGTTCACAGAAACCTTAA 360  
DB 301 AATTATGCGTACAGTATTAAGTATTAATAATAAATCTACAGTTCACAGAAACCTTAA 360  
YY 361 AATCGGTTCGGTGGGACGGTTCATCGGTTTACAGATTTTCAAAATATTCATTGACACT 420  
DB 361 AATCGGTTCGGTGGGACGGTTCATCGGTTTACAGATTTTCAAAATATTCATTGACACT 420  
YY 421 CCTAGTTGGTGTATTAAGTAAATAAGCAGTTTACAGAG 456  
DB 421 CCTAGTTGGTGTATTAAGTAAATAAGCAGTTTACAGAG 456  
RESULT 3  
AAT51749  
ID AAT51749 standard; DNA; 1294 BP.  
AC AAT51749;  
XX AAT51749;  
XX

DT 15-OCT-1997 (first entry)

DE Root cortex specific gene TobRD2 promoter (dell.3).

XX Root cortex-specific promoter; TobRD2; tobacco; transgenic plant;

KW Insecticide; Bacillus thuringiensis; biological control; ss.

XX Nicotiana tabacum.

OS WO9705261-A1.

XX MO9705261-A1.

XX 13-FEB-1997.

PD 24-JUL-1996; 96WO-US12158.

XX 28-JUL-1995; 95US-0508786.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Conkling MA, Mendu N, Song W;

PI WPI: 1997-145698/13.

DR DNA directing heterologous gene expression in the root cortex - used

XX e.g. for expressing insecticidal Bacillus proteins

PS Claim 1; Page 36; 53pp; English.

XX An isolated DNA (AAT51749), designated dell.3, comprises a 1294 bp

CC 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see

CC also AAT51746), which directs root cortex-specific expression of

CC associated genes. Dell.3 can be used in DNA cassettes to direct

CC the expression of heterologous genes in the root cortex layer of

CC transgenic monocot or dicot plants, e.g. Bacillus thuringiensis

CC crystal proteins in tobacco for the control of root-damaging pests.

CC Dell.3 conferred high levels of GUS reporter gene expression

CC (several-fold higher than the CamV35S promoter) in transgenic

CC tobacco root cortex.

XX

XX

SO Sequence 1294 BP; 515 A; 174 C; 203 G; 402 T; 0 other;

Query Match 100.0%; Score 456; DB 18; Length 1294;

Best Local Similarity 100.0%; Pred. No. 4e-68;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAACATATTCATACATTTGTTGCTTCTACTCATTAATCGGTAAATACCTTTGTCCTT 60

DB 265 GGAACATATTCATACATTTGTTGCTTCTACTCATTAATCGGTAAATACCTTTGTCCTT 324

OY 61 GCTAATAAAGATTAAGTGAATAGCTTAAATATTAATTAATGATATTTAGGA 120

DB 325 GCTAATAAAGATTAAGTGAATAGCTTAAATATTAATGATATTTAGGA 384

OY 121 ATTAGTATTTGAGGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180

DB 385 ATTAGTATTTGAGGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 444

OY 181 ATGAAAAATTTAAAGCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240

DB 445 ATGAAAAATTTAAAGCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 504

OY 241 TTTAATCGGTAAAGTGAATAGCTTAAATATTAATTAATTAATTAATTAATTAATTAATTAAT 300

DB 505 TTTAATCGGTAAAGTGAATAGCTTAAATATTAATTAATTAATTAATTAATTAATTAATTAAT 564

OY 301 AATTAATCGGTAAAGTGAATAGCTTAAATATTAATTAATTAATTAATTAATTAATTAATTAAT 360

DB 565 AATTAATCGGTAAAGTGAATAGCTTAAATATTAATTAATTAATTAATTAATTAATTAATTAAT 624

OY 361 AATCGGTTGGTGGGACGGTTCGATCGGTTTAAAGTGAATAGCTTAAATTAATTAATTAATTAAT 420

DB 625 AATCGGTTGGTGGGACGGTTCGATCGGTTTAAAGTGAATAGCTTAAATTAATTAATTAATTAAT 684

OY 421 CCTAGTGTGTATTAAGTAAAAAGCAGTACAGAG 456

DB 685 CCTAGTGTGTATTAAGTAAAAAGCAGTACAGAG 720

RESULT 4

AAT51748

AAT51748 standard; DNA; 1372 BP.

AAT51748;

15-OCT-1997 (first entry)

DE Root cortex specific gene TobRD2 promoter (dell.4).

XX Root cortex-specific promoter; TobRD2; tobacco; transgenic plant;

KW Insecticide; Bacillus thuringiensis; biological control; ss.

XX Nicotiana tabacum.

OS WO9705261-A1.

XX MO9705261-A1.

XX 13-FEB-1997.

PD 24-JUL-1996; 96WO-US12158.

XX 28-JUL-1995; 95US-0508786.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Conkling MA, Mendu N, Song W;

PI WPI: 1997-145698/13.

DR DNA directing heterologous gene expression in the root cortex - used

XX e.g. for expressing insecticidal Bacillus proteins

PS Claim 1; Page 35; 53pp; English.

XX An isolated DNA (AAT51747), designated dell.4, comprises a 1372 bp

CC 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see

CC also AAT51746), which directs root cortex-specific expression of

CC associated genes. Dell.4 can be used in DNA cassettes to direct

CC the expression of heterologous genes in the root cortex layer of

CC transgenic monocot or dicot plants, e.g. Bacillus thuringiensis

CC crystal proteins in tobacco for the control of root-damaging pests.

CC Dell.4 conferred high levels of GUS reporter gene expression

CC (several-fold higher than the CamV35S promoter) in transgenic

CC tobacco root cortex.

XX

XX

SO Sequence 1372 BP; 532 A; 187 C; 215 G; 438 T; 0 other;

Query Match 100.0%; Score 456; DB 18; Length 1372;

Best Local Similarity 100.0%; Pred. No. 3.9e-68;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAACATATTCATACATTTGTTGCTTCTACTCATTAATCGGTAAATACCTTTGTCCTT 60

DB 343 GGAACATATTCATACATTTGTTGCTTCTACTCATTAATCGGTAAATACCTTTGTCCTT 402

OY 61 GCTAATAAAGATTAAGTGAATAGCTTAAATATTAATTAATGATATTTAGGA 120

DB 403 GCTAATAAAGATTAAGTGAATAGCTTAAATATTAATTAATGATATTTAGGA 462

OY 121 ATTAGTATTTGAGGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180

DB 463 ATTAGTATTTGAGGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 522

OY 181 ATGAAAAATTTAAAGCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240

DB 523 ATGAAAAATTTAAAGCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 582

OY 241 TTTAATCGGTAAAGTGAATAGCTTAAATATTAATTAATTAATTAATTAATTAATTAATTAAT 300

Db 583 TTTAATCGGTTAGTTCGATATTTTTCATATTTTATATAAAAATTAACCTTACCCT 642  
 QY 301 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTCTTCAGAAACCTTAA 360  
 Db 643 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTCTTCAGAAACCTTAA 702  
 QY 361 AATCGGTTCCGGTGGGACGGTTCGATCGGTTTGTAGTTCGATTTTCAAAATATTCATTGACACT 420  
 Db 703 AATCGGTTCCGGTGGGACGGTTCGATCGGTTTGTAGTTCGATTTTCAAAATATTCATTGACACT 762  
 QY 421 CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 456  
 Db 763 CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 798

RESULT 5  
 AAT51747 standard; DNA; 1988 BP.  
 AAT51747;

15-OCT-1997 (first entry)

Root cortex specific gene TobRD2 promoter (del2.0).  
 Root cortex specific promoter; TobRD2; tobacco; transgenic plant;  
 Insecticide; Bacillus thuringiensis; biological control; ss.

Nicotiana tabacum.

MO9705261-A1.

13-FEB-1997.

24-JUL-1996; 96WO-US12158.

28-JUL-1995; 95US-0508786.

(UNNC-) UNIV NORTH CAROLINA STATE.

Conkling MA, Mendu N, Song W;

WPI; 1997-145698/13.

DNA directing heterologous gene expression in the root cortex - used  
 e.g. for expressing insecticidal Bacillus proteins

Claim 1; Page 33-34; 53pp; English.

An isolated DNA (AAT51747), designated del2.0, comprises a 1988 bp  
 portion of the tobacco RD2 gene (TobRD2) promoter (see also  
 AAT51746), which directs root cortex-specific expression of  
 associated genes. Del2.0 and truncated TobRD2 promoters (see also  
 AAT51748-56) can be used in DNA cassettes to direct the expression of  
 heterologous genes in the root cortex layer of transgenic monocot  
 or dicot plants, e.g. to express Bacillus thuringiensis crystal  
 proteins in tobacco for the control of root-damaging pests. Del2.0  
 directed high levels of GUS reporter gene expression (4-fold higher  
 than the CAM355 promoter) in transgenic tobacco root cortex.

Sequence 1988 BP; 714 A; 271 C; 302 G; 701 T; 0 other;

Query Match 100.0%; Score 456; DB 18; Length 1988;

Best Local Similarity 100.0%; Pred. No. 3; 8e-68;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACAATATTCATATACATTTGCTACTACTCATATTCGCTGAAATATCTTGTGCTT 60  
 Db 959 GAAACAATATTCATATACATTTGCTACTACTCATATTCGCTGAAATATCTTGTGCTT 1018  
 QY 61 GCTAATAAAGTACTTGAATAAGCTTACTTAAATATTAATAGCATTAATGATTTTACGA 120

Db 1019 GCTAATAAAGTACTTGAATAAGCTTACTTAAATATTAATAGCATTAATGATTTTACGA 1078  
 QY 121 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTCTTCAGAAACCTTAA 180  
 Db 1079 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTCTTCAGAAACCTTAA 1138  
 QY 181 ATGAAAAATTTAAAGCTTTTATAGTTTTAAACTTACTATATATAATTTTTCATATGTA 240  
 Db 1139 ATGAAAAATTTAAAGCTTTTATAGTTTTAAACTTACTATATATAATTTTTCATATGTA 1198  
 QY 241 TTTAATCGGTTAGTTCGATATTTTTCATATTTTATATAAAAATTAACCTTACCCT 300  
 Db 1199 TTTAATCGGTTAGTTCGATATTTTTCATATTTTATATAAAAATTAACCTTACCCT 1258  
 QY 301 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTCTTCAGAAACCTTAA 360  
 Db 1259 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTCTTCAGAAACCTTAA 1318  
 QY 361 AATCGGTTCCGGTGGGACGGTTCGATCGGTTTGTAGTTCGATTTTCAAAATATTCATTGACACT 420  
 Db 1319 AATCGGTTCCGGTGGGACGGTTCGATCGGTTTGTAGTTCGATTTTCAAAATATTCATTGACACT 1378  
 QY 421 CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 456  
 Db 1379 CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 1414

RESULT 6  
 AAT51746 standard; DNA; 2010 BP.  
 AAT51746;

15-OCT-1997 (first entry)

Root cortex specific gene TobRD2 promoter.

Root cortex specific promoter; TobRD2; tobacco; transgenic plant;  
 Insecticide; Bacillus thuringiensis; biological control; ss.

Nicotiana tabacum.

Key Location/Qualifiers

FT TATA\_signal 1971..1975

FT misc\_feature 2000

FT /\*tag- b /note= "predicted start of transcription"

PN MO9705261-A1.

PD 13-FEB-1997.

PE 24-JUL-1996; 96WO-US12158.

PR 28-JUL-1995; 95US-0508786.

PA (UNNC-) UNIV NORTH CAROLINA STATE.

PI Conkling MA, Mendu N, Song W;

DR WPI; 1997-145698/13.

DNA directing heterologous gene expression in the root cortex - used  
 e.g. for expressing insecticidal Bacillus proteins

Claim 1; Page 32-33; 53pp; English.

An isolated DNA (AAT51746) comprises the tobacco RD2 gene (TobRD2)  
 promoter, which directs root cortex-specific expression of  
 associated genes. A clone containing the isolated DNA was obtd.  
 from a tobacco seedling genomic library by screening with TobRD2  
 cDNA. The antisense strand of TobRD2 was used as a probe to show



CC that TobRD2 mRNA is expressed only in the cortex layer of roots.  
 CC truncations of the promoter region (see also AAT51747-54) were prepd.  
 CC by PCR. The full-length or truncated promoters can be used in DNA  
 CC cassettes to direct root cortex-specific expression of heterologous  
 CC genes in transgenic monocot or dicot plants, e.g. to express  
 CC Bacillus thuringiensis crystal proteins in tobacco for the control  
 CC of root-damaging pests.

SO Sequence 2010 BP: 729 A; 276 C; 303 G; 702 T; 0 other;

Query Match 98.9%; Score 451.2; DB 18; Length 2010;  
 Best Local Similarity 99.3%; Pred. No. 2,4e-67;  
 Matches 453; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGAAACATATTCATATACATTTGATGTTGGTACACATTAATGGCTGATTTGCTGCTT 60  
 |||||||  
 Db 959 GGAACATATTCATATACATTTGATGTTGGTACACATTAATGGCTGATTTGCTGCTT 1018  
 OY 61 GCTAAATTAAGATTAAGTAAATGCTTAAATATTAATGATTAATGATTTTAAAGA 120  
 |||||||  
 Db 1019 GCTAAATTAAGATTAAGTAAATGCTTAAATATTAATGATTAATGATTTTAAAGA 1078  
 OY 121 ATTAGTATTTTGGATTAATTAATTAATGATTAATGATTTTAAAGATTTTAAAGA 180  
 |||||||  
 Db 1079 ATTAGTATTTTGGATTAATTAATTAATGATTAATGATTTTAAAGATTTTAAAGA 1138  
 OY 181 ATGAAAAATTAATGCTTTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 240  
 |||||||  
 Db 1139 ATGAAAAATTAATGCTTTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 1198  
 OY 241 TTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 300  
 |||||||  
 Db 1199 TTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 1258  
 OY 301 AATTAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 360  
 |||||||  
 Db 1259 AATTAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 1318  
 OY 361 AATCGGTTGCGTGGGCGGCTTCGATCGGTTGATTTTCAAAATTAATGATTTGACACT 420  
 |||||||  
 Db 1319 AATCGGTTGCGTGGGCGGCTTCGATCGGTTGATTTTCAAAATTAATGATTTGACACT 1378  
 OY 421 CCTAGTTGTTGTTATAGTAAAGCAAGTTACAGAG 456  
 |||||||  
 Db 1379 CCTAGTTGTTGTTATAGTAAAGCAAGTTACAGAG 1414

RESULT 7

AAT51751  
 ID AAT51751 standard; DNA: 722 BP.  
 AC AAT51751;  
 DT 15-OCT-1997 (first entry)  
 DE Root cortex specific gene TobRD2 promoter (del0.7).  
 KW Root cortex-specific promoter; TobRD2; tobacco; transgenic plant;  
 KW Insecticide; Bacillus thuringiensis; biological control; ss.  
 OS Nicotiana tabacum.  
 PN MO9705261-A1.  
 PD 13-FEB-1997.  
 PF 24-JUL-1996; 96MO-US12158.  
 PR 28-JUL-1995; 95US-0508786.  
 PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 PI Conkling MA, Mendu N, Song W;

XX  
 DR WPI: 1997-145698/13.  
 PT DNA directing heterologous gene expression in the root cortex - used  
 PR e.g. for expressing insecticidal Bacillus proteins  
 PS Claim 1; Page 38; 53pp; English.

SO An isolated DNA (AAT51751), designated del0.7, comprises a 722 bp  
 5' deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see  
 CC also AAT51746), which directs root cortex-specific expression of  
 CC associated genes. Del0.7 can be used in DNA cassettes to direct  
 CC the expression of heterologous genes in the root cortex layer of  
 CC transgenic monocot or dicot plants, e.g. Bacillus thuringiensis  
 CC crystal proteins in tobacco for the control of root-damaging pests.  
 CC Del0.7 conferred high levels of GUS reporter gene expression  
 CC (about twice that of the CamV35 promoter) in transgenic tobacco  
 CC root cortex.

SO Sequence 722 BP: 278 A; 107 C; 129 G; 208 T; 0 other;

Query Match 32.5%; Score 148; DB 18; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 309 GTACAGTTATGATTTATATTAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 368  
 |||||||  
 Db 1 GTACAGTTATGATTTATATTAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAT 60  
 OY 369 CGGTGCGGAGCGGTTGCGATTCGATTTTCAAAATTAATGATTTGACACTCCTAGTTG 428  
 |||||||  
 Db 61 CGGTGCGGAGCGGTTGCGATTCGATTTTCAAAATTAATGATTTGACACTCCTAGTTG 120  
 OY 429 TTGTTATAGTAAAGCAAGTTACAGAG 456  
 |||||||  
 Db 121 TTGTTATAGTAAAGCAAGTTACAGAG 148

RESULT 8

ABL32348  
 ID ABL32348 standard; DNA: 5145 BP.  
 AC ABL32348;  
 DT 26-MAR-2002 (first entry)  
 DE Human immune system associated gene SEQ ID NO: 321.  
 KW Human; immune system disease; cytosine methylation; antiastrumatic;  
 KW antiarteriosclerotic; antianemic; cytostatic; nootropic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antirheumatic; antiarthritic; antididiabetic; antiporiatic;  
 KW antifilummatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.  
 XX Homo sapiens.  
 OS WO200200928-A2.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PF 02-JUL-2001; 2001WO-EP07537.  
 PR 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX (EPIC-) EPICENOMICS AG.  
 PA Olek A, Plepenbrock C, Berlin K;  
 PI WPI: 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation

PS Claim 1; SEQ ID NO 321; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, aneama, cancer, acute myeloid leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.

SO Sequence 5145 BP; 1470 A; 27 C; 855 G; 2793 T; 0 other;

Query Match 14.6%; Score 66.6; DB 24; Length 5145;

Best Local Similarity 51.9%; Pred. No. 0.0053;

Matches 176; Conservative 0; Mismatches 159; Indels 4; Gaps 1;

OY 4 AACATATTCAATGATTGTTGGTACCTCATATAAGCGTAGAATACCTTGTGGCTTGTCT 63

Db 511 AATTAATTTTAAAGTTAAAGTTTAAATTTTGGGTATTTATTAATTTGGGTGTTT 570

OY 64 AATTAAGACTCTTGAATAGCTTAAATAATTAATTAATTAAGACTCTTGAATAGCTT 123

Db 571 TATGTTTATGAGGATTAATTAATTTAAATTAATTTAAATGCTTTTAAATTTAAATTT 630

OY 124 AGTATTTGAGTTAAATTAATTTAAATTAATTTAAATTTAAATTTAAATTTAAATTT 183

Db 631 TTTTGTGTTTAAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 686

OY 184 AAAAATTAATGCTTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 243

Db 687 AAAAAGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 746

OY 244 AATCGGATAGTTCGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 303

Db 747 TGTATATATATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 806

OY 304 TATCGGTACGATTAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 342

Db 807 TTTTGTGTTTAAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 845

RESULT 9

ABL34464 standard; DNA; 5145 BP.

ABL34464;

26-MAR-2002 (first entry)

Human metastasis associated gene SEQ ID NO: 17.

Metastasis associated gene; cytosinetic; gene therapy; cancer; cytosine methylation; gene; ds.

Homo sapiens.

WO200177376-A2.

18-OCT-2001.

06-APR-2001; 2001WO-EP03970.

06-APR-2000; 2000DE-1019058.

07-APR-2000; 2000DE-1019173.

30-JUN-2000; 2000DE-1032529.

01-SEP-2000; 2000DE-1043826.

PR

XX

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-010922/01.

PT New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation, also for treatment

PS Claim 1; SEQ ID NO 17; 23pp + Sequence Listing; English.

CC The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.

SO Sequence 5145 BP; 1470 A; 27 C; 855 G; 2793 T; 0 other;

Query Match 14.6%; Score 66.6; DB 24; Length 5145;

Best Local Similarity 51.9%; Pred. No. 0.0053;

Matches 176; Conservative 0; Mismatches 159; Indels 4; Gaps 1;

OY 4 AACATATTCAATGATTGTTGGTACCTCATATAAGCGTAGAATACCTTGTGGCTTGTCT 63

Db 511 AATTAATTTTAAAGTTAAAGTTTAAATTTTGGGTATTTATTAATTTGGGTGTTT 570

OY 64 AATTAAGACTCTTGAATAGCTTAAATAATTAATTAATTAAGACTCTTGAATAGCTT 123

Db 571 TATGTTTATGAGGATTAATTAATTTAAATTAATTTAAATGCTTTTAAATTTAAATTT 630

OY 124 AGTATTTGAGTTAAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 183

Db 631 TTTTGTGTTTAAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 686

OY 184 AAAAATTAATGCTTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 243

Db 687 AAAAAGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 746

OY 244 AATCGGATAGTTCGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 303

Db 747 TGTATATATATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 806

OY 304 TATCGGTACGATTAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 342

Db 807 TTTTGTGTTTAAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 845

RESULT 10

ABL33568/c standard; DNA; 8305 BP.

ABL33568;

26-MAR-2002 (first entry)

Human immune system associated gene SEQ ID NO: 1541.

Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; anti-anemic; cytosinetic; nootropic;

neuroprotective; anti-HIV; antiviral; ophthalmological; anti-inflammatory; cancer; eye disease; arteriosclerosis; anaemia;

acute myeloid leukemia; Alzheimer's disease; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

gene; ds.

Homo sapiens.

WO200200928-A2.

03-JAN-2002.

PR

XX

PF 02-JUL-2001; 2001WO-EP07537.  
 XX 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Plepenbrock C, Berlin K;  
 XX WPI: 2002-130909/17.  
 DR Nucleic acid comprising fragment of chemically modified gene, useful  
 XX for diagnosis and treatment of diseases associated with abnormal  
 XX cytosine methylation -  
 PR Claim 1; SEQ ID NO 1541; 32pp + Sequence Listing; German.  
 PS  
 XX The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 CC  
 XX Sequence 8305 BP; 2181 A; 185 C; 1901 G; 4038 T; 0 other;  
 SQ  
 Query Match 14.6%; Score 66.4; DB 24; Length 8305;  
 Best Local Similarity 49.2%; Pred. No. 0.0056;  
 Matches 175; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

OY 8 TATTCAATRCAGTTGAGTGGTCTACTCAATACCGCTAGAAATCTTGGCCCTGCTAATA 67  
 DB 6424 TATTTAT 6365  
 OY 68 AAGATACCTGAAATATGCTTACTTAAATATATATATATATATATATATATATATATATAT 127  
 DB 6364 AAAAATA 6305  
 OY 128 TTTTGAGTTTAAATTTCTTATTTGACCTGTAACAGTTTTTAAATTTCCAAAGCCCAFGAAAA 187  
 DB 6304 TAAT 6245  
 OY 188 AATTTAATGCTTTATATGTTTAAACTTACTATATATATATATATATATATATATATATAT 247  
 DB 6244 AAT 6185  
 OY 248 GGTATAGTTGCAATTTTTTCAATTTTATATATATATATATATATATATATATATATAT 307  
 DB 6184 TAAT 6125  
 OY 308 GGTACAGTTATAGATTTTAAATATATATATATATATATATATATATATATATATATAT 363  
 DB 6124 TAT 6069

RESULT 11  
 ABL33307  
 ID ABL33307 standard; DNA; 6175 BP.  
 AC ABL33307;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DE Human immune system associated gene SEQ ID NO: 1280.  
 XX  
 XX Human; immune system disease; cytosine methylation; antiasthmatic;  
 KM antiarteriosclerotic; antihaemic; cytosinatic; noctropic;  
 KM neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;  
 KM antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KM antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KM gene; ds.  
 XX Homo sapiens.  
 OS WO200200928-A2.  
 XX  
 XX 03-JAN-2002.  
 XX  
 XX 02-JUL-2001; 2001WO-EP07537.  
 XX  
 XX 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX  
 XX (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Plepenbrock C, Berlin K;  
 XX WPI: 2002-130909/17.  
 DR Nucleic acid comprising fragment of chemically modified gene, useful  
 XX for diagnosis and treatment of diseases associated with abnormal  
 XX cytosine methylation -  
 PR Claim 1; SEQ ID NO 1280; 32pp + Sequence Listing; German.  
 PS  
 XX The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 CC  
 XX Sequence 6175 BP; 1506 A; 154 C; 1357 G; 3158 T; 0 other;  
 SQ  
 Query Match 13.4%; Score 61; DB 24; Length 6175;  
 Best Local Similarity 48.7%; Pred. No. 0.046;  
 Matches 166; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

OY 7 AATTTCAATACCTGTTAGTGGTCTACTCAATATCCGCTAGAAATCTTGGCCCTGCTAAT 66  
 DB 4615 AAT 4674  
 OY 67 AAAAGTACTTGAATATGCTTACTTAAATATATATATATATATATATATATATATATATAT 126  
 DB 4675 AAT 4734  
 OY 127 AATTTGAGTTTAAATTTCTTATTTGACCTGTAACAGTTTTTAAATTTCCAAAGCCCAFGAAAA 186  
 DB 4735 TGTAT 4794  
 OY 187 AATTTAATGCTTTATATGTTTAAACTTACTATATATATATATATATATATATATATATAT 246  
 DB 4795 GTTTAAATTTAT 4854  
 OY 247 CGGTATAGTTGCAATTTTTTCAATTTTATATATATATATATATATATATATATATATAT 306  
 DB 4855 AATTTAATGCTTTATATGTTTAAACTTACTATATATATATATATATATATATATATAT 4914  
 OY 307 CGGTACAGTTATAGATTTTAAATATATATATATATATATATATATATATATATATATAT 347  
 DB 4915 GTATTTAT 4955

RESULT 12  
 ABR33948  
 ID ABR33948 standard; DNA; 18997 BP.  
 AC ABR33948;  
 XX  
 XX 18-JUN-2002 (first entry)

Human DNA for staging of Astrocytomas #16.

Human; ds; astrocytoma; cytosatic; staging; cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry.

Homo sapiens.

WO200202808-A2.

10-JAN-2002.

02-JUL-2001; 2001WO-EP07538.

30-JUN-2000; 2000DE-1033529.

01-SEP-2000; 2000DE-1043826.

(EPIG-) EPIGENOMICS AG.

Olek A, Plepenbrock C, Berlin K;

WPI: 2002-171649/22.

Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to astrocytomas

Claim 1; SEQ ID NO 31; 37pp; English.

The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ABK33919-ABK34032) or its complement. Also included are an oligonucleotide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), primers for (I), probes for detecting cytosine methylation or single-nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the methylation status of the CpG dinucleotides of (I). The array is useful for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated genomic DNA fragments using the array and a polymerase, where the amplification carries a detectable label. The method further involves identifying methylation status of one or more cytosine positions, and analysing methylation status of the cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplification step amplifies DNA which is of particular interest in astrocytoma or brain tissue, based on the specific genomic methylation status of brain tissues, as opposed to background DNA. The amplification carries a fluorescent label or radioclabel. Optionally, the labels of the amplification are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Preferably, the amplification or fragments of the amplification are detected by matrix assisted laser desorption/ionisation mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The present sequence is one of the chemically pre-treated reference DNA samples of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pcl\_sequences.

Query Match 13.2%; Score 60.4; DB 24; Length 18997;

Best Local Similarity 49.7%; Pred. No. 0.053;

Matches 154; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

19 TTGTAGTTTCTACTCATAAATCGTAGAATCTTGTCCCTTGTCAATTAAGATCTTGA 78

13515 TTGAGCTTTTCTTAAATTTTGTGGGATTTTGTATTAATTTTGAATAATTTGG 13574

79 AATAGCTTAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 138

13575 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13634

139 AATAGCTTAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 198

13635 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 13694

199 TATTAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 258

13695 TATTAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13754

259 AATAGCTTAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 318

13755 AATAGCTTAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13814

319 AGATTTAATAT 328

13815 GATTTGTTTT 13824

RESULT 13

ABL32570

ID ABL32570 standard; DNA; 18997 BP.

XX XX

AC ABL32570;

XX XX

DT 26-MAR-2002 (first entry)

XX XX

DE Human immune system associated gene SEQ ID NO: 543.

XX XX

KW Human; immune system disease; cytosine methylation; antiasthmatic;

XX XX

OS antidiarrhoeal; anti-nausea; antiemetic; cytosatic; noctropic;

XX XX

KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

XX XX

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;

XX XX

KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

XX XX

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

XX XX

gene; ds.

OS Homo sapiens.

XX XX

WO200200928-A2.

XX XX

03-JAN-2002.

XX XX

02-JUL-2001; 2001WO-EP07537.

XX XX

30-JUN-2000; 2000DE-1033529.

XX XX

01-SEP-2000; 2000DE-1043826.

XX XX

(EPIG-) EPIGENOMICS AG.

XX XX

Olek A, Plepenbrock C, Berlin K;

XX XX

WPI: 2002-130909/17.

XX XX

Nucleic acid comprising fragment of chemically modified gene, useful

XX XX

PT for diagnosis and treatment of diseases associated with abnormal

XX XX

PR cytosine methylation

XX XX

PS Claim 1; SEQ ID NO 543; 32pp + Sequence Listing; German.

XX XX

CC The present invention provides a number of human immune system associated

CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.

XX Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;

Query Match 13.2%; Score 60.4; DB 24; Length 18997;

Best Local Similarity 49.7%; Pred. No. 0.053;

Matches 154; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 19 TTGTAGTTGGCTACGATCATATCCGGAGAAATGCTTGGCCCTGCTAATAAAGATPACTTGA 78
13515 TTGAGGTTTTTTTTTAAATTTTGTGGGATTTTGGATTTATATGTTTTTAAATTAATTTGG 13574

QY 79 AATAGCTTACGTTAAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 138
13575 TTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13634

QY 139 ATACTTATGACTGTAACAGCTTTTAAATTCACAGCCCGCATGAAAATTTTAAATGCTT 198
13635 TTAAATGAT 13694

QY 139 TATTGTTTTTAACTTACTATATAAATTTTCATATGTAATAATTTTATCGGTATAGTTCG 258
13695 TATTTTAAATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 13754

QY 259 ATATTTTTTCAATTTTATTTTAAATTAATAAATTAATTAATTAATTAATTAATTAATTAAT 318
13755 APTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13814

QY 319 AGATTTAAT 328
13815 GATTTGTTTT 13824

RESULT 14

ABL33576
ABL33576 standard; DNA; 5925 BP.

ABL33576;

26-MAR-2002 (first entry)

Human immune system associated gene SEQ ID NO: 1549.

Human; immune system disease; cytosine methylation; antiasthmatic;
antiartherosclerotic; anti-amyloid; anti-anemic; anti-epileptic;
anti-inflammatory; anti-rheumatic; anti-arthritic; anti-diabetic; anti-psoriasis;
anti-infective; anti-cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
gene; ds.

Homo sapiens.
WO200200928-A2.

03-JAN-2002.

02-JUL-2001; 2001WO-EP07537.

30-JUN-2000; 2000DE-1032529.

01-SEP-2000; 2000DE-1043826.

(EPig-) EPIGENOMICS AG.
Olek A, Plepenbrock C, Berlin K;

DR WPI: 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful
PR for diagnosis and treatment of diseases associated with abnormal
PR cytosine methylation

XX Claim 1; SEQ ID NO 1549; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.

XX Sequence 5925 BP; 1510 A; 105 C; 1246 G; 3064 T; 0 other;

Query Match 13.2%; Score 60.2; DB 24; Length 5925;

Best Local Similarity 50.9%; Pred. No. 0.062;

Matches 143; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 65 APTAAGAATCTGAAATAGCTTATGATTTAAATGATGATGATGATGATGATGATGATGATGAT 124
2199 APTAAGGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 2258

QY 125 GATTTTGGCTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 184
2259 GATTTTGGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 2318

QY 185 AAAAAATTAATGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 244
2319 GGTATTTAATAAGTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 2378

QY 245 ATCGGTAATGCTGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 304
2379 APTAAGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 2438

QY 305 ATCGGTACAGTTATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 345
2439 GATTTTGGTGTGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 2479

RESULT 15

ABL33569
ABL33569 standard; DNA; 8305 BP.

ABL33569;

26-MAR-2002 (first entry)

Human immune system associated gene SEQ ID NO: 1542.

Human; immune system disease; cytosine methylation; antiasthmatic;
antiartherosclerotic; anti-amyloid; anti-anemic; anti-epileptic;
anti-inflammatory; anti-rheumatic; anti-arthritic; anti-diabetic; anti-psoriasis;
anti-infective; anti-cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
gene; ds.

Homo sapiens.
WO200200928-A2.

03-JAN-2002.

02-JUL-2001; 2001WO-EP07537.

30-JUN-2000; 2000DE-1032529.

01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.  
 PA  
 XX  
 PI Olek A, Plepenbrock C, Berlin K;  
 XX  
 DR WPI: 2002-130909/17.  
 XX

PT Nucleic acid comprising fragment of chemically modified gene, useful  
 for diagnosis and treatment of diseases associated with abnormal  
 cytosine methylation  
 PI  
 XX  
 PS Claim 1; SEQ ID NO 1542; 32pp + sequence listing; German.  
 XX

CC The present invention provides a number of human immune system associated  
 genes which are modified by the methylation of cytosines. The sequences  
 can be used in the diagnosis and treatment of immune system disorders,  
 including eye diseases such as retinopathy, neovascular glaucoma and  
 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 diseases. The present sequence is a gene of the invention.  
 CC  
 XX

SQ Sequence 8305 BP; 2163 A; 185 C; 2060 G; 3897 T; 0 other;

Query Match 13.2%; Score 60; DB 24; Length 8305;  
 Best Local Similarity 48.0%; Pred. No. 0.066;  
 Matches 171; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

OY 8 TATTCGAATACATTGTGATTTGGCTACTCATTAATCGCTAGAAATCTTTGGCTTAAATA 67  
 DB 1882 TATTTATATATAAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1941  
 OY 68 AAGATACCTGAAATAGCTTACTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 127  
 DB 1942 AGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2001  
 OY 128 TTTTGAGTTTAACTTACTTATTTGACTTTGAAAGTTTAAATTTCCAAAGCCCATGAATA 187  
 DB 2002 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2061  
 OY 188 ATTAAATGCTTTTATTAAGTTTAACTTAACTTAAATTAATTTTCCATATGTAATAATTAATC 247  
 DB 2062 AATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2121  
 OY 248 GGTATAGTTCGATATTTTTCATTTTAAATTAATTAATTAATTAATTAATTAATTAATC 307  
 DB 2122 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2181  
 OY 308 GGTACAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 363  
 DB 2182 TATATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2237

Search completed: June 9, 2003, 07:16:39  
 Job time : 192 secs

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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:13:20 ; Search time 44 Seconds  
(without alignments)  
3178.286 Million cell updates/sec

Title: US-09-941-042C-1

Perfect score: 456 1 ggaacatcattcaatcatt.....gtaaaagcagttacagag 456

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Issued\_Patents\_MA:\*
- 2: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/BACKFILES1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	100.0	1030	US-08-508-786-5	Sequence 5, Appl1
2	456	100.0	1030	PCT-US96-12158-5	Sequence 5, Appl1
3	456	100.0	1294	US-08-508-786-4	Sequence 4, Appl1
4	456	100.0	1294	PCT-US96-12158-4	Sequence 4, Appl1
5	456	100.0	1372	US-08-508-786-3	Sequence 3, Appl1
6	456	100.0	1372	PCT-US96-12158-3	Sequence 3, Appl1
7	456	100.0	1988	US-08-508-786-2	Sequence 2, Appl1
8	456	100.0	1988	PCT-US96-12158-2	Sequence 2, Appl1
9	456	100.0	2010	US-08-508-786-1	Sequence 1, Appl1
10	456	100.0	2010	PCT-US96-12158-1	Sequence 1, Appl1
11	148	32.5	722	US-08-508-786-6	Sequence 6, Appl1
12	148	32.5	722	PCT-US96-12158-6	Sequence 6, Appl1
13	60.8	13.3	837	US-08-998-416-288	Sequence 288, App
14	59.4	13.0	20674	US-09-641-638-651	Sequence 651, App
15	55.6	12.2	636	US-08-998-416-1137	Sequence 1137, App
16	52.8	11.6	615	US-08-998-416-1186	Sequence 186, App
17	52.8	11.6	1850	US-08-617-860B-32	Sequence 32, App
18	52.8	11.6	4098	US-08-605-106-4	Sequence 4, Appl1
19	52.6	11.5	319	US-07-593-657-14	Sequence 14, Appl1
20	52.6	11.5	1241	US-07-593-657-6	Sequence 6, Appl1
21	52.6	11.5	1241	US-08-942-012B-3	Sequence 3, Appl1
22	51.4	11.3	665	US-08-883-795A-36	Sequence 36, Appl1
23	51.4	11.3	3618	US-07-872-678A-36	Sequence 36, Appl1
24	51.4	11.3	724	US-08-998-416-683	Sequence 683, App
25	50.8	11.2	724	US-08-998-416-683	Sequence 683, App
26	49.8	10.9	665	US-08-883-795A-36	Sequence 36, Appl1
27	49.2	10.8	5108	US-09-056-075-1	Sequence 1, Appl1
				US-09-306-446C-8	Sequence 8, Appl1

Result No.	Score	Query Match	Length	DB ID	Description
28	48.6	10.7	5852	US-07-867-106-2	Sequence 2, Appl1
29	48.6	10.7	8920	US-08-446-855A-1	Sequence 1, Appl1
30	48.6	10.7	8920	US-09-150-741-1	Sequence 1, Appl1
31	48.4	10.6	19124	US-08-487-826B-13	Sequence 13, Appl1
32	48.4	10.6	20674	US-09-641-638-651	Sequence 651, App
33	47.8	10.5	854	US-08-998-416-534	Sequence 534, App
34	47.8	10.5	854	US-08-998-416-534	Sequence 534, App
35	47.8	10.5	860	US-08-998-416-287	Sequence 287, App
36	47.4	10.4	663	US-08-213-419B-3	Sequence 3, Appl1
37	47.4	10.4	19124	US-08-487-826B-13	Sequence 13, Appl1
38	47.2	10.4	615	US-08-998-416-186	Sequence 186, App
39	47.2	10.4	51952	US-08-947-823-1	Sequence 1, Appl1
40	47	10.3	8920	US-08-446-855A-1	Sequence 1, Appl1
41	47	10.3	8920	US-09-150-741-1	Sequence 1, Appl1
42	46.8	10.3	162450	US-09-345-882-1	Sequence 1, Appl1
43	46.6	10.2	7521	US-09-004-838-116	Sequence 116, App
44	46.4	10.2	636	US-08-998-416-1137	Sequence 1137, App
45	46.4	10.2	837	US-08-998-416-288	Sequence 288, App

ALIGNMENTS

```

RESULT 1
US-08-508-786-5
: Sequence 5, Application US/08508786
: Patent No. 5837876
GENERAL INFORMATION:
APPLICANT: ConKling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Kenneth D. Sibley, Bell, Seltzer, Park 6
ADDRESS: Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5837876th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508, 786
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-508-786-5
Query Match 100.0%; Score 456; DB 2; Length 1030;
Best Local Similarity 100.0%; Pred. No. 5.5e-85;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAACAATATTCATACATGTAAGTGTGATTTGCTACATATGATGCTGATGCTGCTT 60
Db 1 GGAACAATATTCATACATGTAAGTGTGATTTGCTACATATGATGCTGATGCTGCTT 60

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QY 61 GGTAAATAAGACTCTGGAATAGCTTACTGTTAAATATAATGCAATATGATTTTGA 120
DB 61 GGTAAATAAGACTCTGGAATAGCTTACTGTTAAATATAATGCAATATGATTTTGA 120
QY 121 ATTACTATTTTGGAGTTTAAATTAAGTACTGTTAAACGTTTAAATATCCAAAGGCC 180
DB 121 ATTACTATTTTGGAGTTTAAATTAAGTACTGTTAAACGTTTAAATATCCAAAGGCC 180
QY 181 ATGAAAAATTTAAATGCTTATTAAGTTTAAACCTATATATAATTTTTCATATGTA 240
DB 181 ATGAAAAATTTAAATGCTTATTAAGTTTAAACCTATATATAATTTTTCATATGTA 240
QY 241 TTTAATCGGTATAGTTCGATATTTTTCATATTTTAAATATAATTTTAAATCC 300
DB 241 TTTAATCGGTATAGTTCGATATTTTTCATATTTTAAATATAATTTTAAATCC 300
QY 301 AATTCGGTACAGTTATAGATTTTAAATATAATTTTAAATATAATTTTAAATCC 360
DB 301 AATTCGGTACAGTTATAGATTTTAAATATAATTTTAAATATAATTTTAAATCC 360
QY 361 AATCGGTTCGGTTCGCGAGCGTTCGATTCGTTTTCGATTTTCAATATTTGACACT 420
DB 361 AATCGGTTCGGTTCGCGAGCGTTCGATTCGTTTTCGATTTTCAATATTTGACACT 420
QY 421 CCTAGTTGTTGTTATAGGTTAAATAAGCAAGTTCACAGAG 456
DB 421 CCTAGTTGTTGTTATAGGTTAAATAAGCAAGTTCACAGAG 456

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RESULT 2

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PCT-US96-12158-5
; Sequence 5, Application PC/TUS9612158
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark A.
; APPLICANT: Mendu, Nandini
; APPLICANT: Song, Men
; TITLE OF INVENTION: Root Cortex Specific Gene Promoter
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kenneth D. Sibley; Bell, Seltzer, Park &
; ADDRESS: Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: North Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12158
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3175
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1030 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US96-12158-5
Query Match 100.0%; Score 456; DB 5; Length 1030;

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Best Local Similarity 100.0%; Pred. No. 5.5e-85;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAACATATTCATACATTTGAGTTGGCTACTCATTAATCCGTAGAAATCTTGGCC 60
DB 1 GGAACATATTCATACATTTGAGTTGGCTACTCATTAATCCGTAGAAATCTTGGCC 60
QY 61 GCTAATAAAGACTCTGGAATAGCTTACTGTTAAATATAATGCAATATGATTTTGA 120
DB 61 GCTAATAAAGACTCTGGAATAGCTTACTGTTAAATATAATGCAATATGATTTTGA 120
QY 121 ATTACTATTTTGGAGTTTAAATTAAGTACTGTTAAACGTTTAAATATCCAAAGGCC 180
DB 121 ATTACTATTTTGGAGTTTAAATTAAGTACTGTTAAACGTTTAAATATCCAAAGGCC 180
QY 181 ATGAAAAATTTAAATGCTTATTAAGTTTAAACCTATATATAATTTTTCATATGTA 240
DB 181 ATGAAAAATTTAAATGCTTATTAAGTTTAAACCTATATATAATTTTTCATATGTA 240
QY 241 TTTAATCGGTATAGTTCGATATTTTTCATATTTTAAATATAATTTTAAATCC 300
DB 241 TTTAATCGGTATAGTTCGATATTTTTCATATTTTAAATATAATTTTAAATCC 300
QY 301 AATTCGGTACAGTTATAGATTTTAAATATAATTTTAAATATAATTTTAAATCC 360
DB 301 AATTCGGTACAGTTATAGATTTTAAATATAATTTTAAATATAATTTTAAATCC 360
QY 361 AATCGGTTCGGTTCGCGAGCGTTCGATTCGTTTTCGATTTTCAATATTTGACACT 420
DB 361 AATCGGTTCGGTTCGCGAGCGTTCGATTCGTTTTCGATTTTCAATATTTGACACT 420
QY 421 CCTAGTTGTTGTTATAGGTTAAATAAGCAAGTTCACAGAG 456
DB 421 CCTAGTTGTTGTTATAGGTTAAATAAGCAAGTTCACAGAG 456

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RESULT 3

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US-08-508-786-4
; Sequence 4, Application US/08508786
; Patent No. 5837876
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark A.
; APPLICANT: Mendu, Nandini
; APPLICANT: Song, Men
; TITLE OF INVENTION: Root Cortex Specific Gene Promoter
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kenneth D. Sibley; Bell, Seltzer, Park &
; ADDRESS: Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5837876th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,786
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3175
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1294 base pairs

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TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-508-786-4

Query Match 100.0%; Score 456; DB 2; Length 1294;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-85;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAACATATTCAATGATTTGTTGCTTCTGACGATTAATTCGATGAGTACTTGTGCGCTT 60  
 |||  
 DB 265 GGAACATATTCAATGATTTGTTGCTTCTGACGATTAATTCGATGAGTACTTGTGCGCTT 324  
 |||  
 DB 61 GCTAAATAAAGATPACTTGAATAATAGCTTAATTAATAATAATAGCATTAATGATTTTGA 120  
 |||  
 DB 325 GCTAAATAAAGATPACTTGAATAATAGCTTAATTAATAATAATAGCATTAATGATTTTGA 384  
 |||  
 OY 121 ATTAGATTTTGGATTTAATTTACTTTTATGACCTTGAACAGTTTATTAATTCGAAAGGCC 180  
 |||  
 DB 385 ATTAGATTTTGGATTTAATTTACTTTTATGACCTTGAACAGTTTATTAATTCGAAAGGCC 444  
 |||  
 OY 181 ATGAAAAATTTAATGCTTTATTTATGTTTTAAACTTACTATATTAATTTTCATATGTAAAA 240  
 |||  
 DB 445 ATGAAAAATTTAATGCTTTATTTATGTTTTAAACTTACTATATTAATTTTCATATGTAAAA 504  
 |||  
 OY 241 TTTAAATCGGTATGATTTGATTTTCAATTTTATTTTAAAAAATAAATAAATTAACCTTACCCT 300  
 |||  
 DB 505 TTTAAATCGGTATGATTTGATTTTCAATTTTATTTTAAAAAATAAATAAATTAACCTTACCCT 564  
 |||  
 OY 301 AATTTATCGGTACGATTTATGATTTTATATAAAAATTAACGTTCTCAGAAGAAACCTAAA 360  
 |||  
 DB 565 AATTTATCGGTACGATTTATGATTTTATATAAAAATTAACGTTCTCAGAAGAAACCTAAA 624  
 |||  
 OY 361 AATCGGTTCCGTCGGACGGGATGATGCGTTAGTCGATTTCAAAATTAATTCATTTGACACT 420  
 |||  
 DB 625 AATCGGTTCCGTCGGACGGGATGATGCGTTAGTCGATTTCAAAATTAATTCATTTGACACT 684  
 |||  
 OY 421 CCTAGTTGTTTATATAGGTAAAAAGCAGTTACAGAG 456  
 |||  
 DB 685 CCTAGTTGTTTATATAGGTAAAAAGCAGTTACAGAG 720  
 |||

RESULT 4

PCT-US96-12158-4  
 ; Sequence 4, Application PC/US9612158  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conkling, Mark A.  
 ; APPLICANT: Mendu, Nandini  
 ; APPLICANT: Song, Wen  
 ; TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &  
 ; STREET: Post Office Drawer 34009  
 ; CITY: Charlotte  
 ; STATE: North Carolina  
 ; COUNTRY: USA  
 ; ZIP: 28234  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/12158  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sibley, Kenneth D.  
 ; REGISTRATION NUMBER: 31,665  
 ; REFERENCE/DOCKET NUMBER: 5051-294

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1294 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 PCT-US96-12158-4

Query Match 100.0%; Score 456; DB 5; Length 1294;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-85;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAACATATTCAATGATTTGTTGCTTCTGACGATTAATTCGATGAGTACTTGTGCGCTT 60  
 |||  
 DB 265 GGAACATATTCAATGATTTGTTGCTTCTGACGATTAATTCGATGAGTACTTGTGCGCTT 324  
 |||  
 OY 61 GCTAAATAAAGATPACTTGAATAATAGCTTAATTAATAATAATAGCATTAATGATTTTGA 120  
 |||  
 DB 325 GCTAAATAAAGATPACTTGAATAATAGCTTAATTAATAATAATAGCATTAATGATTTTGA 384  
 |||  
 OY 121 ATTAGATTTTGGATTTAATTTACTTTTATGACCTTGAACAGTTTATTAATTCGAAAGGCC 180  
 |||  
 DB 385 ATTAGATTTTGGATTTAATTTACTTTTATGACCTTGAACAGTTTATTAATTCGAAAGGCC 444  
 |||  
 OY 181 ATGAAAAATTTAATGCTTTATTTATGTTTTAAACTTACTATATTAATTTTCATATGTAAAA 240  
 |||  
 DB 445 ATGAAAAATTTAATGCTTTATTTATGTTTTAAACTTACTATATTAATTTTCATATGTAAAA 504  
 |||  
 OY 241 TTTAAATCGGTATGATTTGATTTTCAATTTTATTTTAAAAAATAAATAAATTAACCTTACCCT 300  
 |||  
 DB 505 TTTAAATCGGTATGATTTGATTTTCAATTTTATTTTAAAAAATAAATAAATTAACCTTACCCT 564  
 |||  
 OY 301 AATTTATCGGTACGATTTATGATTTTATATAAAAATTAACGTTCTCAGAAGAAACCTAAA 360  
 |||  
 DB 565 AATTTATCGGTACGATTTATGATTTTATATAAAAATTAACGTTCTCAGAAGAAACCTAAA 624  
 |||  
 OY 361 AATCGGTTCCGTCGGACGGGATGATGCGTTAGTCGATTTCAAAATTAATTCATTTGACACT 420  
 |||  
 DB 625 AATCGGTTCCGTCGGACGGGATGATGCGTTAGTCGATTTCAAAATTAATTCATTTGACACT 684  
 |||  
 OY 421 CCTAGTTGTTTATATAGGTAAAAAGCAGTTACAGAG 456  
 |||  
 DB 685 CCTAGTTGTTTATATAGGTAAAAAGCAGTTACAGAG 720  
 |||

RESULT 5

US-08-508-786-3  
 ; Sequence 3, Application US/08508786  
 ; Patent No. 5837876  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conkling, Mark A.  
 ; APPLICANT: Mendu, Nandini  
 ; APPLICANT: Song, Wen  
 ; TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &  
 ; STREET: Post Office Drawer 34009  
 ; CITY: Charlotte  
 ; STATE: No. 5837876th Carolina  
 ; COUNTRY: USA  
 ; ZIP: 28234  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/508,786  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sibley, Kenneth D.  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5051-294  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1372 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-508-786-3

Query Match 100.0%; Score 456; DB 2; Length 1372;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-85;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGAACAATTCATACATGTTGCTCTACTCTAATTCGCTAGAAATACCTTTGTCCTT 60
   |||
Db 343 GGAACAATTCATACATGTTGCTCTACTCTAATTCGCTAGAAATACCTTTGTCCTT 402
   |||
OY 61 GCTAATAAAGACTCTGAATAAGCTTAGTTAAATATATATAGCATATATAGATTTTAGA 120
   |||
Db 403 GCTAATAAAGACTCTGAATAAGCTTAGTTAAATATATATAGCATATATAGATTTTAGA 462
   |||
OY 121 AATGATATTTGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180
   |||
Db 463 AATGATATTTGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 522
   |||
OY 181 ATGAAAAATTAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
   |||
Db 523 ATGAAAAATTAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 582
   |||
OY 241 TTTAATCGGTATGATGATATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTC 300
   |||
Db 583 TTTAATCGGTATGATGATATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTC 642
   |||
OY 301 AATTAATCGGTACAGTTATATATATATATATATATATATATATATATATATATATATAT 360
   |||
Db 643 AATTAATCGGTACAGTTATATATATATATATATATATATATATATATATATATATATAT 702
   |||
OY 361 AATGCGTTCGGTGGGAGCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGT 420
   |||
Db 703 AATGCGTTCGGTGGGAGCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGT 762
   |||
OY 421 CCTAGTTGTTTATAGGTTAAAGACAGTTACAGAG 456
   |||
Db 763 CCTAGTTGTTTATAGGTTAAAGACAGTTACAGAG 798
   |||
  
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RESULT 6  
 PCT-US96-12158-3  
 Sequence 3, Application PC/TUS9612158  
 GENERAL INFORMATION:  
 APPLICANT: Conkling, Mark A.  
 APPLICANT: Mendu, Nandini  
 APPLICANT: Song, Wen  
 TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
 ADDRESS: Gibson  
 STREET: Post Office Drawer 34009  
 CITY: Charlotte  
 STATE: North Carolina  
 COUNTRY: USA  
 ZIP: 28234

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/12158  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sibley, Kenneth D.  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5051-294  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1372 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 PCT-US96-12158-3

Query Match 100.0%; Score 456; DB 5; Length 1372;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-85;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 GGAACAATTCATACATGTTGCTCTACTCTAATTCGCTAGAAATACCTTTGTCCTT 60
   |||
Db 343 GGAACAATTCATACATGTTGCTCTACTCTAATTCGCTAGAAATACCTTTGTCCTT 402
   |||
OY 61 GCTAATAAAGACTCTGAATAAGCTTAGTTAAATATATATAGCATATATAGATTTTAGA 120
   |||
Db 403 GCTAATAAAGACTCTGAATAAGCTTAGTTAAATATATATAGCATATATAGATTTTAGA 462
   |||
OY 121 AATGATATTTGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180
   |||
Db 463 AATGATATTTGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 522
   |||
OY 181 ATGAAAAATTAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
   |||
Db 523 ATGAAAAATTAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 582
   |||
OY 241 TTTAATCGGTATGATGATATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTC 300
   |||
Db 583 TTTAATCGGTATGATGATATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTC 642
   |||
OY 301 AATTAATCGGTACAGTTATATATATATATATATATATATATATATATATATATATATAT 360
   |||
Db 643 AATTAATCGGTACAGTTATATATATATATATATATATATATATATATATATATATATAT 702
   |||
OY 361 AATGCGTTCGGTGGGAGCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGT 420
   |||
Db 703 AATGCGTTCGGTGGGAGCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGTTCGATCGT 762
   |||
OY 421 CCTAGTTGTTTATAGGTTAAAGACAGTTACAGAG 456
   |||
Db 763 CCTAGTTGTTTATAGGTTAAAGACAGTTACAGAG 798
   |||
  
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RESULT 7  
 US-08-508-786-2  
 Sequence 2, Application US/08508786  
 Patent No. 5837876  
 GENERAL INFORMATION:  
 APPLICANT: Conkling, Mark A.  
 APPLICANT: Mendu, Nandini  
 APPLICANT: Song, Wen  
 TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:

```

ADDRESS: Kenneth D. Sibley, Bell, Seltzer, Park &
ADDRESS: Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 583786th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-508-786-2

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Query Match 100.0%; Score 456; DB 2; Length 1988;
Best Local Similarity 100.0%; Pred. No. 5.8e-85;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACAATATTCATACATTTGATGTTGGCTACTCATTAATCGTAGAATTAAGTGGCTT 60
DB 959 GGAACAATATTCATACATTTGATGTTGGCTACTCATTAATCGTAGAATTAAGTGGCTT 1018
QY 61 GCTAAATPAAAGATGACTTGAATAGCTTAAATATTAATTAATGATGATTTTAAAGGA 120
DB 1019 GCTAAATPAAAGATGACTTGAATAGCTTAAATATTAATTAATGATGATTTTAAAGGA 1078
QY 121 ATTAGATTTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
DB 1079 ATTAGATTTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1138
QY 181 ATGAAAAATTTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 240
DB 1139 ATGAAAAATTTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 1198
QY 241 TTTAATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 300
DB 1199 TTTAATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 1258
QY 301 AATTATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 360
DB 1259 AATTATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 1318
QY 361 AATCGGTTCCGGTGGGACGGTTTCGATCGGTTTAAATTAATTAATTAATTAATTAATTAAT 420
DB 1319 AATCGGTTCCGGTGGGACGGTTTCGATCGGTTTAAATTAATTAATTAATTAATTAATTAAT 1378
QY 421 CCTAGTTGTTGTTATAGGTAATAAAGACGTTACAGAG 456
DB 1379 CCTAGTTGTTGTTATAGGTAATAAAGACGTTACAGAG 1414

```

```

APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Kenneth D. Sibley, Bell, Seltzer, Park &
ADDRESS: Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: North Carolina
ZIP: 28234
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-12158-2

Query Match 100.0%; Score 456; DB 5; Length 1988;
Best Local Similarity 100.0%; Pred. No. 5.8e-85;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACAATATTCATACATTTGATGTTGGCTACTCATTAATCGTAGAATTAAGTGGCTT 60
DB 959 GGAACAATATTCATACATTTGATGTTGGCTACTCATTAATCGTAGAATTAAGTGGCTT 1018
QY 61 GCTAAATPAAAGATGACTTGAATAGCTTAAATATTAATTAATGATGATTTTAAAGGA 120
DB 1019 GCTAAATPAAAGATGACTTGAATAGCTTAAATATTAATTAATGATGATTTTAAAGGA 1078
QY 121 ATTAGATTTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
DB 1079 ATTAGATTTTGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1138
QY 181 ATGAAAAATTTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 240
DB 1139 ATGAAAAATTTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 1198
QY 241 TTTAATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 300
DB 1199 TTTAATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 1258
QY 301 AATTATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 360
DB 1259 AATTATCGGATTAATGCTTTATTTAGTTTAAACTTACTATTAATTAATTAATTAATTAAT 1318
QY 361 AATCGGTTCCGGTGGGACGGTTTCGATCGGTTTAAATTAATTAATTAATTAATTAATTAAT 420
DB 1319 AATCGGTTCCGGTGGGACGGTTTCGATCGGTTTAAATTAATTAATTAATTAATTAATTAAT 1378
QY 421 CCTAGTTGTTGTTATAGGTAATAAAGACGTTACAGAG 456
DB 1379 CCTAGTTGTTGTTATAGGTAATAAAGACGTTACAGAG 1414

```

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RESULT 8
PCT-US96-12158-2
; Sequence 2, Application PC/TUS9612158
; GENERAL INFORMATION:

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04/11/03

RESULT 9

US-08-508-786-1  
Sequence 1, Application US/08508786  
Patent No. 5837876  
GENERAL INFORMATION:  
APPLICANT: Conkling, Mark A.  
APPLICANT: Mendu, Nandini  
APPLICANT: Song, Wen  
TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
ADDRESS: Gldson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5837876th Carolina  
COUNTRY: USA  
ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508.786  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2010 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

Query Match 100.0%; Score 456; DB 2; Length 2010;  
Best Local Similarity 100.0%; Pred. No. 5.8e-85;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Table with 4 columns: ID, Sequence, Score, Length. Rows include query sequence (1) and database matches (959, 61, 1019, 121, 1079, 181, 1139, 241, 1199, 301, 1259).

RESULT 10

PCT-US96-12158-1  
Sequence 1, Application PC/TUS9612158  
GENERAL INFORMATION:  
APPLICANT: Conkling, Mark A.  
APPLICANT: Mendu, Nandini  
APPLICANT: Song, Wen  
TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
ADDRESS: Gldson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: North Carolina  
COUNTRY: USA  
ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12158  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2010 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

Query Match 100.0%; Score 456; DB 5; Length 2010;  
Best Local Similarity 100.0%; Pred. No. 5.8e-85;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Table with 4 columns: ID, Sequence, Score, Length. Rows include query sequence (1) and database matches (959, 61, 1019, 121, 1079, 181, 1139, 241).

Db 1199 TTTAAATCGGTATAGTTCGATATTTTTTCAATTTATTTTAAATAAAAAAAGCTTACCCT 1258  
 QY 301 AATTAATCGGTACAGTTATATAGATTTATATAAAAAATCTACGGTCTCGAAGAAACCTAAA 360  
 Db 1259 AATTAATCGGTACAGTTATATAGATTTATATAAAAAATCTACGGTCTCGAAGAAACCTAAA 1318  
 QY 361 AATCGGTTCGGTCGACGAGCGTTCGATCGGTTTATAGTCCATTTTCAAAATATTCATTCAGACT 420  
 Db 1319 AATCGGTTCGGTCGACGAGCGTTCGATCGGTTTATAGTCCATTTTCAAAATATTCATTCAGACT 1378  
 QY 421 CCTAGTTGTTGTTATATAGGTTAAAAAGCAGTTACAGAG 456  
 Db 1379 CCTAGTTGTTGTTATATAGGTTAAAAAGCAGTTACAGAG 1414

*01200003*

RESULT 11  
 US-08-786-6  
 ? Sequence 6, Application US/08508786  
 ? Patent No. 5837876  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Conkling, Mark A.  
 ? APPLICANT: Mendu, Nandini  
 ? TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 ? NUMBER OF SEQUENCES: 9  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
 ? ATTORNEY/AGENT INFORMATION:  
 ? STREET: Post Office Drawer 34009  
 ? CITY: Charlotte  
 ? STATE: NO. 5837876th Carolina  
 ? COUNTRY: USA  
 ? ZIP: 28234  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/508,786  
 ? FILING DATE:  
 ? CLASSIFICATION: 800  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Sibley, Kenneth D.  
 ? REGISTRATION NUMBER: 31,665  
 ? REFERENCE/DOCKET NUMBER: 5051-294  
 ? TELEPHONE: 919-420-2200  
 ? TELEFAX: 919-881-3175  
 ? INFORMATION FOR SEQ ID NO: 6:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 722 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: DNA (genomic)  
 ? US-08-508-786-6

Query Match 32.5%; Score 148; DB 2; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 2,6e-22;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GTACAGTTATAGATTTATATAAAAAATCTACGGTCTTCAGAGAAACCTAAAAATCGGTT 368  
 Db 1 GTACAGTTATAGATTTATATAAAAAATCTACGGTCTTCAGAGAAACCTAAAAATCGGTT 60  
 QY 369 CGGTGCGGACGGTTCGATCGGTTTATAGTCCATTTTCAAAATATTCATTCAGACT 428  
 Db 61 CGGTGCGGACGGTTCGATCGGTTTATAGTCCATTTTCAAAATATTCATTCAGACT 120  
 QY 429 TTGTTATAGGTTAAAAAGCAGTTACAGAG 456  
 Db 121 TTGTTATAGGTTAAAAAGCAGTTACAGAG 148

RESULT 12  
 PCT-US96-12158-6  
 ? Sequence 6, Application PC/IUS9612158  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Conkling, Mark A.  
 ? APPLICANT: Mendu, Nandini  
 ? TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 ? NUMBER OF SEQUENCES: 9  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
 ? ATTORNEY/AGENT INFORMATION:  
 ? STREET: Post Office Drawer 34009  
 ? CITY: Charlotte  
 ? STATE: North Carolina  
 ? COUNTRY: USA  
 ? ZIP: 28234  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: PCT/US96/12158  
 ? FILING DATE:  
 ? CLASSIFICATION:  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Sibley, Kenneth D.  
 ? REGISTRATION NUMBER: 31,665  
 ? REFERENCE/DOCKET NUMBER: 5051-294  
 ? TELEPHONE: 919-420-2200  
 ? TELEFAX: 919-881-3175  
 ? INFORMATION FOR SEQ ID NO: 6:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 722 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: DNA (genomic)  
 ? PCT-US96-12158-6

Query Match 32.5%; Score 148; DB 5; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 2,6e-22;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GTACAGTTATAGATTTATATAAAAAATCTACGGTCTTCAGAGAAACCTAAAAATCGGTT 368  
 Db 1 GTACAGTTATAGATTTATATAAAAAATCTACGGTCTTCAGAGAAACCTAAAAATCGGTT 60  
 QY 369 CGGTGCGGACGGTTCGATCGGTTTATAGTCCATTTTCAAAATATTCATTCAGACT 428  
 Db 61 CGGTGCGGACGGTTCGATCGGTTTATAGTCCATTTTCAAAATATTCATTCAGACT 120  
 QY 429 TTGTTATAGGTTAAAAAGCAGTTACAGAG 456  
 Db 121 TTGTTATAGGTTAAAAAGCAGTTACAGAG 148

RESULT 13  
 US-08-998-416-288  
 ? Sequence 288, Application US/08998416  
 ? Patent No. 6239264  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Pohlmann, Peter  
 ? APPLICANT: Steiner, Sabine  
 ? APPLICANT: Mohr, Christlne  
 ? APPLICANT: Wendland, Jurgen  
 ? APPLICANT: Knechtle, Philipp  
 ? APPLICANT: Reblischung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTIPII  
 AND USES THEREOF  
 NUMBER OF SEQUENCES: 1152  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 6239264artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: No. 6239264th Carolina  
 COUNTRY: USA  
 ZIP: 27709

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/998,416  
 FILING DATE: 24-DEC-1997  
 CLASSIFICATION: 435  
 PRIORITY DATA:  
 PRIORITY APPLICATION NUMBER: CH 0016/97  
 FILING DATE: 31-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
 TELEPHONE: 919-541-8587  
 TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 288:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 837 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: PLAGI241RP  
 US-08-998-416-288

Query Match 13.3%; Score 60.6; DB 4; Length 837;  
 Best Local Similarity 51.1%; Pred. No. 0.00016;  
 Matches 168; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

QY 4 AACCAATTCATTAACATTCGTTAGCTTGCATCATATCCGCTGAGAACTTTGCTGCT 63  
 DB 234 AAAATTAGTATTAATAAATTTATTTAGATTTATTTATTTCTTTAAATTTAAATGA 293

QY 64 AATAAGATTAAGTAAATAGCTTGTGTTAAATATTAATAGATTAAGATTTAGGAAT 123  
 DB 294 TTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 353

QY 124 AGTATTTGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 181  
 DB 354 TAAAGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 413

QY 182 TGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 241  
 DB 414 TAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 473

QY 242 TTATTCGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 301  
 DB 474 TTATTCGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 533

QY 302 ATTAATTCGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 330  
 DB 534 TTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 562

RESULT 14  
 ; Sequence 651, Application US/09641638  
 ; Patent No. 6432648

GENERAL INFORMATION:  
 APPLICANT: Blumenfeld, Marta  
 APPLICANT: Bougenlelet, Lydie  
 APPLICANT: Chumakov, Ilya  
 APPLICANT: Cohen, Annick  
 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
 FILE REFERENCE: GENSET.051CP1  
 CURRENT APPLICATION NUMBER: US/09/641,638  
 PRIORITY FILING DATE: 2000-08-16  
 PRIOR APPLICATION NUMBER: US 09/502,330  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: US 60/133,200  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: US 09/275,267  
 PRIOR FILING DATE: 1999-03-23  
 PRIOR APPLICATION NUMBER: US 60/119,917  
 PRIOR FILING DATE: 1999-02-12  
 NUMBER OF SEQ ID NOS: 1304  
 SOFTWARE: Patent.pm  
 SEQ ID NO 651  
 LENGTH: 20674

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1123..3123  
 OTHER INFORMATION: 5' regulatory region

NAME/KEY: exon  
 LOCATION: 3124..3297  
 OTHER INFORMATION: exon 1

NAME/KEY: exon  
 LOCATION: 3871..4072  
 OTHER INFORMATION: exon 2

NAME/KEY: exon  
 LOCATION: 5552..5633  
 OTHER INFORMATION: exon 3

NAME/KEY: exon  
 LOCATION: 5758..5880  
 OTHER INFORMATION: exon 4

NAME/KEY: exon  
 LOCATION: 5996..6099  
 OTHER INFORMATION: exon 5

NAME/KEY: exon  
 LOCATION: 6349..6509  
 OTHER INFORMATION: exon 6

NAME/KEY: exon  
 LOCATION: 7379..7522  
 OTHER INFORMATION: exon 7

NAME/KEY: exon  
 LOCATION: 8645..8854  
 OTHER INFORMATION: exon 8

NAME/KEY: exon  
 LOCATION: 12254..12340  
 OTHER INFORMATION: exon 9

NAME/KEY: exon  
 LOCATION: 12854..13023  
 OTHER INFORMATION: exon 10

NAME/KEY: exon  
 LOCATION: 13308..13429  
 OTHER INFORMATION: exon 11

NAME/KEY: exon  
 LOCATION: 16567..16667  
 OTHER INFORMATION: exon 12

NAME/KEY: exon  
 LOCATION: 16775..16945  
 OTHER INFORMATION: exon 13

NAME/KEY: exon  
 LOCATION: 17063..17554  
 OTHER INFORMATION: exon 14

NAME/KEY: misc\_feature  
 LOCATION: 17555..20674  
 OTHER INFORMATION: 3' regulatory region



OY 291 ACTTACCCCTAATTTATGCGTACAGTTTATAGATTATATATATAAANAACCTACGGTCTCCAGAA 350  
 DB 11304 ATTTAACCTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 11363  
 OY 351 GAACCTPA 359  
 DB 11364 TTAATTTA 11372

RESULT 15

US-08-998-416-1137  
 ; Sequence 1137 Application US/08998416  
 ; Patent No. 6239264

GENERAL INFORMATION:  
 APPLICANT: Philippesen, Peter  
 APPLICANT: Pohlmann, Rainer  
 APPLICANT: Stehner, Sabine  
 APPLICANT: Mohr, Christine  
 APPLICANT: Wendland, Jurgen  
 APPLICANT: Knechtle, Philipp  
 APPLICANT: Reblschung, Corinne  
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
 NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:  
 ADDRESS: No. 6239264artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: No. 62392644th Carolina  
 COUNTRY: USA  
 ZIP: 27709

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 435  
 FILING DATE: 24-DEC-1997

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: CH 0016/97  
 FILING DATE: 31-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meligs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/GCC1976  
 TELEPHONE: 919-541-8587  
 TELEFAX: 919-541-8689  
 INFORMATION FOR SEQ ID NO: 1137:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 636 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: PAB1692RP  
 US-08-998-416-1137

Query Match 12.2%; Score 55.6; DB 4; Length 636;  
 Best Local Similarity 52.1%; Pred. No. 0.0016;  
 Matches 148; Conservative 0; Mismatches 134; Indels 2; Gaps 1;

OY 4 AACATATTCATACATATTGATGTTGCTACAGCATATAATGCTAGAAATGCTGTCCTGCT 63  
 DB 234 AAATTAAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 293  
 OY 64 AATAAAGATACCTGAATAGCTTAAATATAAATAAGATAGATTGATTTGGAAT 123  
 DB 294 TTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATAAAATAATTAATA 353

OY 124 AGTATTTTGTAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 181  
 DB 354 TAAAGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 413  
 OY 182 TGAATAATTTAAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 241  
 DB 414 TAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 473  
 OY 242 TTAATCGGTATAGTTCCATATTTTTCATTTTAAATTAATTAATA 285  
 DB 474 TTAACCTTAATTTCTTATTAATTAATTAATTAATTAATTAATA 517

Search completed: June 9, 2003, 08:04:35  
 Job time : 46 secs



GenCore version 5.1.6  
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OW nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:10:45 ; Search time 125 Seconds  
(Without alignments)  
5105.512 Million cell updates/sec

Title: US-09-941-042c-1  
Perfect score: 456  
Sequence: 1 ggaacataatcacaatt.....ggtcaaaagcgttacaagag 456

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 3: /cgn2\_6/ptoddata/1/pubpna/US06\_NEM\_PUB.seq:\*\*
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  - 8: /cgn2\_6/ptoddata/1/pubpna/US08\_PUBCOMB.seq:\*\*
  - 9: /cgn2\_6/ptoddata/1/pubpna/US09\_NEM\_PUB.seq:\*\*
  - 10: /cgn2\_6/ptoddata/1/pubpna/US09\_PUBCOMB.seq:\*\*
  - 11: /cgn2\_6/ptoddata/1/pubpna/US10\_NEM\_PUB.seq:\*\*
  - 12: /cgn2\_6/ptoddata/1/pubpna/US10\_PUBCOMB.seq:\*\*
  - 13: /cgn2\_6/ptoddata/1/pubpna/US60\_NEM\_PUB.seq:\*\*
  - 14: /cgn2\_6/ptoddata/1/pubpna/US60\_PUBCOMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.2	12.8	858	US-10-198-846-7035	Sequence 7035, Ap
2	57	12.5	53332	US-10-224-562-3	Sequence 3, Appl1
3	57	12.5	53332	US-09-801-861-3	Sequence 3, Appl1
4	54.4	11.9	6327	US-10-239-676-151	Sequence 151, App
5	53.6	11.8	14078	US-08-781-986A-191	Sequence 191, App
6	53.4	11.8	513509	US-09-754-853A-4	Sequence 4, Appl1
7	53.4	11.7	272	US-09-969-373-607	Sequence 607, App
8	53.4	11.7	272	US-09-969-373-608	Sequence 608, App
9	53	11.6	6030	US-10-239-676-164	Sequence 164, App
10	53	11.6	15732	US-10-239-676-96	Sequence 96, Appl
11	52.8	11.6	11047	US-10-239-676-187	Sequence 187, App
12	52.6	11.5	3991	US-10-074-045-60	Sequence 60, Appl
13	52.4	11.5	4985	US-10-094-240-10	Sequence 10, Appl
14	52.2	11.4	3991	US-10-074-045-60	Sequence 60, Appl
15	52	11.4	376	US-09-960-352-5087	Sequence 5087, Ap
16	51.6	11.3	640681	US-09-790-988-1	Sequence 1, Appl1
17	51.4	11.3	7380	US-10-239-676-66	Sequence 66, Appl
18	51.4	11.3	17421	US-10-239-676-54	Sequence 54, Appl
19	51.2	11.2	2000	US-09-938-842A-3652	Sequence 3652, Ap

Result No.	Score	Query Match	Length	DB ID	Description
20	50.6	11.1	9515	US-10-239-676-159	Sequence 159, App
21	50.4	11.1	640681	US-09-790-988-1	Sequence 1, Appl1
22	50.2	11.0	7823	US-10-239-676-197	Sequence 197, App
23	50	11.0	419	US-09-960-352-11234	Sequence 11234, A
24	50	11.0	5689	US-10-239-676-90	Sequence 90, Appl
25	49.6	10.9	414	US-09-960-352-6528	Sequence 6528, App
26	49.6	10.9	437	US-09-969-373-937	Sequence 937, App
27	49.6	10.9	335913	US-09-754-853A-2	Sequence 2, Appl1
28	49.6	10.9	335913	US-09-754-853A-3	Sequence 3, Appl1
29	49.4	10.8	424	US-10-198-846-2929	Sequence 2929, App
30	49.4	10.8	11036	US-10-239-676-118	Sequence 118, App
31	49.4	10.8	15732	US-10-239-676-95	Sequence 95, Appl
32	49.4	10.8	15732	US-10-239-676-96	Sequence 96, Appl
33	49	10.7	960	US-10-198-846-6381	Sequence 6381, App
34	49	10.7	4187	US-10-072-349-252	Sequence 252, App
35	49	10.7	4187	US-09-764-855-252	Sequence 252, App
36	48.8	10.7	5979	US-10-239-676-18	Sequence 18, Appl
37	48.8	10.7	6306	US-10-239-676-223	Sequence 223, App
38	48.8	10.7	6815	US-10-239-676-50	Sequence 50, Appl
39	48.8	10.7	7038	US-10-239-676-204	Sequence 204, App
40	48.6	10.7	714	US-10-060-036-256	Sequence 256, App
41	48.6	10.7	7089	US-10-239-676-67	Sequence 67, Appl
42	48.6	10.7	8842	US-10-239-676-71	Sequence 71, Appl
43	48.4	10.6	12405	US-10-239-676-36	Sequence 36, Appl
44	48.4	10.6	12003	US-09-764-877-3976	Sequence 3976, Ap
45	48.4	10.6	30350	US-10-118-328-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1  
US-10-198-846-7035/c  
Sequence 7035, Application US/10198846  
Publication No. US2003099974A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Xu, Yongyao  
APPLICANT: Wang, Youzhen  
APPLICANT: Steinmann, Kathleen  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
FILE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MRI-049  
CURRENT APPLICATION NUMBER: US/10/198,846  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/306,220  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14084  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 7035  
LENGTH: 858  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 137, 182, 183, 184, 185, 186, 187, 188, 189, 209, 211, 212, 217,  
LOCATION: 219, 224, 225, 236, 237, 238, 240, 241, 242, 248, 250, 252,  
LOCATION: 253, 259, 276, 279, 281, 294, 298, 304, 306, 318, 319,  
LOCATION: 320, 321, 327, 338, 349, 350, 352, 353, 363, 378, 379  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 380, 386, 389, 392, 398, 399, 400, 408, 410, 414, 434, 441,  
LOCATION: 443, 446, 451, 453, 466, 488, 490, 497, 498, 499, 501, 503,  
LOCATION: 506, 509, 513, 517, 526, 527, 528, 529, 536, 550, 557, 562,  
LOCATION: 564, 565, 573, 576, 588, 599, 604, 607, 616, 617, 619  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 627, 628, 643, 649, 661, 666, 672, 680, 689, 698, 706, 719,  
LOCATION: 722, 735, 739, 750, 763, 765, 769, 771, 772, 774, 784, 787,  
LOCATION: 790, 791, 792, 795, 798, 805, 814, 816, 819, 820, 822, 830,

```

; SEQ ID NO 151
; LENGTH: 6327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-151

```

```

Query Match 11.9%; Score 54.4; DB 9; Length 6327;
Best Local Similarity 54.5%; Pred. No. 1.9;
Matches 109; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

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QY 138 AATTAAGTATTTGACCTGTGTAACAGCTTTTATTAATCCAGGCCCATGAAATTTAATGCT 197
DB 2900 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2841
QY 198 TATTAAGTATTTAAACCTGATATTAATTTTTCATATGTAATTTAATCGGATATGCT 257
DB 2840 TATTAAGTATTTTCCGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2781
QY 258 GATATTTTTCATTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 317
DB 2780 TATTAAGTATTTTATTTTACCTTTACAAAATTAATTAATTAATTAATTAATTAATTA 2721
QY 318 TAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 337
DB 2720 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2701

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RESULT 5

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US-08-781-986A-191
; Sequence 191, Application US/08781986A
; Publication No. US20030054436A1

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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5253
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 14078 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-191

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Query Match 11.8%; Score 53.6; DB 7; Length 14078;
Best Local Similarity 46.7%; Pred. No. 3.2;

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Matches 170; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

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QY 4 AACATATTCATTAACATTTGATTTGCTACTCAATATCGTAGAATACCTTTGGCTTGC 63
DB 11440 AACCAAGTCCACCTCCATCCACATTTTGAATTAATTAATTAATTAATTAATTAAT 11499
QY 64 AATTAAGATTAAGTAAATGAAATGCTTAAATTAATTAATTAATTAATTAATTAATTA 123
DB 11500 TTACAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 11559
QY 124 AGTATTTTGGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 183
DB 11560 AATTAAGACACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 11619
QY 184 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 243
DB 11620 AATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 11679
QY 244 AATGCGTATGATGATATTTTTCATTTTAAATTAATTAATTAATTAATTAATTAAT 303
DB 11680 AATTAAGTATTTGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 11739
QY 304 TATCGTACAGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 363
DB 11740 TAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 11799
QY 364 CGGT 367
DB 11800 AGGT 11803

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RESULT 6

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US-09-754-853A-4/c
; Sequence 4, Application US/09754853A
; Publication No. US20030005491A1

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GENERAL INFORMATION:
APPLICANT: Haughe, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Mang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(13810)B
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US/09/754,853A
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 4
LENGTH: 513509
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (111805)..(113968), (114684)..(115204)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4

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Query Match 11.8%; Score 53.6; DB 9; Length 513509;
Best Local Similarity 57.9%; Pred. No. 9.1;
Matches 95; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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QY 122 TTAGTATTTGAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 181
DB 136361 TTATGTTTAAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13630
QY 182 TGAATAATTTAATGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 241
DB 136301 GTCAACAATTTAAACATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 13624

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QY 242 TTAATCGGTATGTCATATTTTTTTTCAATTTAATAAA 285
    | | | | | | | | | | | | | | | | | | | | |
Db 136241 ATTGCATTTTAAAGTCTATATAATGTCACAAATTTGTTATCATCTATTATA 136198

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RESULT 7
US-09-969-373-607/C
: Sequence 607, Application US/09969373
: Patent No. US20020133852A1
: GENERAL INFORMATION:
: APPLICANT: Eferetz, Roger J.
: APPLICANT: Hauge, Brian M.
: TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
: FILE REFERENCE: 38-10(52679)A
: CURRENT APPLICATION NUMBER: US/09/969,373
: PRIOR FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: US 09/754,853
: PRIOR FILING DATE: 2001-01-05
: PRIOR APPLICATION NUMBER: US 09/760,427
: PRIOR FILING DATE: 2001-01-13
: PRIOR APPLICATION NUMBER: US 09/855,768
: NUMBER OF SEQ ID NOS: 4593
: LENGTH: 272
: TYPE: DNA
: ORGANISM: Glycine max
US-09-969-373-607

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Query Match 11.7%; Score 53.4; DB 10; Length 272:
Best Local Similarity 50.6%; Pred. No. 1.1;
Matches 129; Conservative 0; Mismatches 126; Indels 0; Gaps 0:
QY 90 TTAATATATTAATAGCATATATATTTTGAATATGATTTTTTGAATTAATACTATTG 149
  | | | | | | | | | | | | | | | | | | | | |
Db 255 TTAATAATTAATATATATTTTAATTAATTTTTCCTTCAATTTAAGTTGTTAA 196
QY 150 ACTTGTAACAGTTTATTAATTCAGGCCCGCATGAAATTTAATGCTTATTAGTTTA 209
  | | | | | | | | | | | | | | | | | | | | |
Db 195 AATATATATGATTTTCTATTATTTTAAAGTTTAAATTAATGACCAATTTAATTA 136
QY 210 ACTTACTATATAATTTTTGATATGTAATTAACGCGATATGTCGATTTTCA 269
  | | | | | | | | | | | | | | | | | | | | |
Db 135 TTATTTTAAATTAATTTAAATTCCTTAAAGTCTCAAAATTTAAGTCCTTAA 76
QY 270 ATTATTTTTTAAATTAATTAATTCCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 329
  | | | | | | | | | | | | | | | | | | | | |
Db 75 AACATTTATTTTCATGTATTTATTTTGTGAATTTATACCTGTTTATTTTAAATTTGAATC 16
QY 330 AAAATCTACGGTCT 344
  | | | | | | | | | | | | | | | | | | | | |
Db 15 ACATTTGAAGGTTCT 1

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RESULT 8
US-09-969-373-608/C
: Sequence 608, Application US/09969373
: Patent No. US20020133852A1
: GENERAL INFORMATION:
: APPLICANT: Eferetz, Roger J.
: APPLICANT: Hauge, Brian M.
: TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
: FILE REFERENCE: 38-10(52679)A
: CURRENT APPLICATION NUMBER: US/09/969,373
: PRIOR FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: US 09/754,853
: PRIOR FILING DATE: 2001-01-05
: PRIOR APPLICATION NUMBER: US 09/760,427
: PRIOR FILING DATE: 2001-01-13
: PRIOR APPLICATION NUMBER: US 09/855,768
: PRIOR FILING DATE: 2001-05-15
: NUMBER OF SEQ ID NOS: 4593

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: SEQ ID NO 608
: LENGTH: 272
: TYPE: DNA
: ORGANISM: Glycine max
US-09-969-373-608

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Query Match 11.7%; Score 53.4; DB 10; Length 272:
Best Local Similarity 50.6%; Pred. No. 1.1;
Matches 129; Conservative 0; Mismatches 126; Indels 0; Gaps 0:
QY 90 TTAATATATTAATAGCATATATATTTTGAATATGATTTTTTGAATTAATACTATTG 149
  | | | | | | | | | | | | | | | | | | | | |
Db 255 TTAATAATTAATATATATTTTAATTAATTTTTCCTTCAATTTAAGTTGTTAA 196
QY 150 ACTTGTAACAGTTTATTAATTCAGGCCCGCATGAAATTTAATGCTTATTAGTTTA 209
  | | | | | | | | | | | | | | | | | | | | |
Db 195 AATATATGATTTTCTATTATTTTAAAGTTTAAATTAATGACCAATTTAATTA 136
QY 210 ACTTACTATATAATTTTTGATATGTAATTAACGCGATATGTCGATTTTCA 269
  | | | | | | | | | | | | | | | | | | | | |
Db 135 TTATTTTAAATTAATTTAAATTCCTTAAAGTCTCAAAATTTAAGTCCTTAA 76
QY 270 ATTATTTTTTAAATTAATTAATTCCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 329
  | | | | | | | | | | | | | | | | | | | | |
Db 75 AACATTTATTTTCATGTATTTATTTTGTGAATTTATACCTGTTTATTTTAAATTTGAATC 16
QY 330 AAAATCTACGGTCT 344
  | | | | | | | | | | | | | | | | | | | | |
Db 15 ACATTTGAAGGTTCT 1

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RESULT 9
US-10-239-676-164
: Sequence 164, Application US/10239676
: Publication No. US20030082609A1
: GENERAL INFORMATION:
: APPLICANT: OLER, Alexander
: APPLICANT: PIEPENROCK, Christian
: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
: FILE REFERENCE: 5013.1003
: CURRENT APPLICATION NUMBER: US/10/239,676
: PRIOR FILING DATE: 2002-09-24
: PRIOR APPLICATION NUMBER: PCT/EP01/03968
: DE 10019173.8
: DE 10032529.7
: DE 10043826.1
: PRIOR FILING DATE: 2001-04-06
: 2000-04-06
: 2000-04-07
: 2000-06-30
: 2000-09-01
: NUMBER OF SEQ ID NOS: 228
: SEQ ID NO 164
: LENGTH: 6030
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: NAME/KEY: unsure
: LOCATION: (5455)
US-10-239-676-164

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```

Query Match 11.6%; Score 53; DB 9; Length 6030;
Best Local Similarity 48.0%; Pred. No. 3.2;
Matches 181; Conservative 0; Mismatches 195; Indels 1; Gaps 1;
QY 80 ATAGCTTAGTTTAATTAATTAATGCAATTAATAGATTGATTTTGGAGTTTA 139
  | | | | | | | | | | | | | | | | | | | | |
Db 704 ATGATTTTAAATGATTTAGTTTGTAGTTTGAATTAAGAAATTTGAGTTTGAATTA 763

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140 TTAGCTATGACTTGTAAACAGTTTAAATTCCAGCCGCGGCAAAATTAATGCTTT 199  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 764 TTTTAAATTTTAAATTTTAAATTAAGATTAATGAATTAATAAATTAATTTTAAAAATTTT 823  
 QY 200 ATTGGTTTAACTTACTATATATAATTTTTCATATATGAAATTTAAATTCGGATATGTTCA 259  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 824 TTTTATTTTAAATTTTAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 883  
 QY 260 TATTTTCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 319  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 884 TTTGAAATTTACCGCTTTTGTGTTATTTATTTAATTTAATTTATTTGTTGTGTTAAAGATA 943  
 QY 320 GATTTAATATAAATACTAAGCTCTCTCAAGAAACCCTAAAATCGGTTCCGGGCGGACG 379  
 Db 944 TAAATAAAGAGTTGTAAAAATTTATTTAGTAGTAGGAATAATAATTTGATTTTATTTTGG 1003  
 QY 380 GTTCGA-TCGGTTATGCGATTTTCCAAATTTCCATTTGCACTCCTGCTGTTGTTAAATG 438  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1004 GTTTAAGGAAGTATGTTTTTGTAGTATTAATTAATTAATTAATTTATTTGTTATTTAT 1063  
 QY 439 TAAAAGGAGTTACAGA 455  
 Db 1064 TTAGTGAAATTTGAGA 1080

RESULT 10  
 US-10-239-676-96  
 ; Sequence 96, Application US/10239676  
 ; Publication No. US20030082609A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIPENBROCK, Christian  
 ; APPLICANT: BERLIN, Kurt  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation  
 ; FILE REFERENCE: 5013.1003  
 ; CURRENT APPLICATION NUMBER: US/10/239.676  
 ; PRIOR FILING DATE: 2002-09-24  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03968

DE 10019058.8  
 DE 10019173.8  
 DE 10032529.7  
 DE 10043826.1  
 PRIOR FILING DATE: 2001-04-06  
 2000-04-06  
 2000-04-07  
 2000-06-30  
 2000-09-01  
 NUMBER OF SEQ ID NOS: 228  
 SEQ ID NO 96  
 LENGTH: 15732  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-239-676-96

Query Match 11.6%; Score 53; DB 9; Length 15732;  
 Best Local Similarity 46.6%; Pred. No. 4.2; Indels 0; Gaps 0;  
 Matches 170; Conservative 0; Mismatches 195; Indels 0; Gaps 0;  
 QY 71 ATACTGAAAATGCTTAGTTAAATTAATTAATGCAATTAATGAGATTTTAGGAATTAGATTTT 130  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 15182 AATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15241  
 QY 131 TCAATTTAACTTAATGACCTTTAACAAGTTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTT 190  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 15242 TTAATATTAATGATTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 15301  
 QY 191 TAAATGCTTAACTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 250  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 15302 AATGTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15361  
 QY 251 AATAGTTGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 310

15362 ATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 15421  
 QY 311 ACAGTTATGATTTTAATAAATACTACGGTTCTTCAGAAACCTAAAAATCGGTTTCG 370  
 Db 15422 TTTGAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 15481  
 QY 371 GTGGGAGCGTTGCATCGTTTACGATTTTTCATTAATTTAATTTAATTTAATTTTAAATTTTAA 430  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 15482 GTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 15541  
 QY 431 GTTAT 435  
 Db 15542 TTTT 15546

RESULT 11  
 US-10-239-676-187  
 ; Sequence 187, Application US/10239676  
 ; Publication No. US20030082609A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIPENBROCK, Christian  
 ; APPLICANT: BERLIN, Kurt  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation  
 ; FILE REFERENCE: 5013.1003  
 ; CURRENT APPLICATION NUMBER: US/10/239.676  
 ; PRIOR FILING DATE: 2002-09-24  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03968

DE 10019058.8  
 DE 10019173.8  
 DE 10032529.7  
 DE 10043826.1  
 PRIOR FILING DATE: 2001-04-06  
 2000-04-06  
 2000-04-07  
 2000-06-30  
 2000-09-01  
 NUMBER OF SEQ ID NOS: 228  
 SEQ ID NO 187  
 LENGTH: 11047  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-239-676-187

Query Match 54.7%; Score 52.8; DB 9; Length 11047;  
 Best Local Similarity 102; Indels 5; Gaps 1;  
 Matches 129; Conservative 0; Mismatches 102; Indels 5; Gaps 1;  
 QY 51 TTTTGCCTTGCTAAATTAATTAATGATTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 110  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 7767 TTTGTGATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 7826  
 QY 111 GATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 170  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 7827 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 7886  
 QY 171 TCCAAGCCCAAGAAAATTTAATGCTTTATTTAATTTAATTTAATTTAATTTAATTTTAAATTTT 230  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 7887 TTGAATTTTTCGTAGATTTT-----TTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 7941  
 QY 231 AATAGTAAATTTAAATCGGATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 286  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 7942 GTATATGATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 7997  
 RESULT 12  
 US-10-074-045-60  
 ; Sequence 60, Application US/10074045  
 ; Publication No. US2003009210ZAI  
 ; GENERAL INFORMATION:

```

; LENGTH: 376
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB3058-032-Q1-K1-F9
US-09-960-352-5087

```

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Query Match 11.48; Score 52; DB 10; Length 376;
Best Local Similarity 52.38; Pred. No. 2.1;
Matches 115; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

```

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QY 68 AAGTACTTGAATAGCTTAGTTAAATATAATAGCATAATAGATTTAGGAATAGTA 127
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 100 AATAATATATTTATTTACATTCATTTAAATATTTTAAATTTTGATTAATA 159
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 128 TTTGAGTTAATTAATTAATGACTTGTAAACAGTTTAAATTCAGCCCAAGAAA 187
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 160 TTTTATTTTATTTATTTATTTTGTATTTTATTTTATTTTATTTATTTAT 219
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 188 ATTTAATGCTTTATTTAGTTTAACTTACTATATATAATTTTTCATATGTA 247
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 220 TTTTAAATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTT 279
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 248 GGTATAGTTCATATTTTTCATATTTTAAATA 287
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 280 ATTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 319
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Search completed: June 9, 2003, 08:03:40
Job time : 127 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:10:15 ; Search time 1128 Seconds  
(Without alignments)  
6547.112 Million cell updates/sec

Title: US-09-941-042c-1  
Perfect score: 456  
Sequence: 1 ggaacataatcacaatc.....gtaaaagcagttacagag 456

Scoring table: IDENTITY\_NMC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: em\_estbda:\*\*
- 2: em\_esthbm:\*\*
- 3: em\_esthnm:\*\*
- 4: em\_esthnm:\*\*
- 5: em\_esthnm:\*\*
- 6: em\_esthnm:\*\*
- 7: em\_esthnm:\*\*
- 8: em\_esthnm:\*\*
- 9: gb\_estl1:\*\*
- 10: gb\_estl2:\*\*
- 11: gb\_estl3:\*\*
- 12: gb\_estl4:\*\*
- 13: gb\_estl5:\*\*
- 14: gb\_estl6:\*\*
- 15: em\_esthnm:\*\*
- 16: em\_esthnm:\*\*
- 17: gb\_estl1:\*\*
- 18: em\_gss\_hum:\*\*
- 19: em\_gss\_inv:\*\*
- 20: em\_gss\_pln:\*\*
- 21: em\_gss\_vrt:\*\*
- 22: em\_gss\_fun:\*\*
- 23: em\_gss\_mam:\*\*
- 24: em\_gss\_mus:\*\*
- 25: em\_gss\_other:\*\*
- 26: em\_gss\_pro:\*\*
- 27: em\_gss\_rtd:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.2	16.5	1101	17	CNS00FYG
2	74.8	16.4	905	17	CNS00KHX
3	73.2	16.1	928	17	CNS00DKY
4	72.6	15.9	976	17	CNS04ESM
5	72.6	15.9	1101	17	CNS00EVL
6	72.6	15.9	1225	17	CNS0161D

Result No.	Score	Query Match	Length	DB ID	Description
7	72	15.8	928	17	CNS00DKY
8	71.2	15.6	987	17	CNS014PQ
9	70.2	15.4	1101	17	CNS00LTP
10	69.2	15.2	1101	17	CNS016L1
11	69.2	15.2	1043	17	CNS0145P
12	68.4	15.0	987	17	CNS014PQ
13	68.4	15.0	1203	17	CNS015WD
14	68.2	15.0	1101	17	CNS00E07
15	68.2	14.9	1101	17	CNS001PB
16	67.6	14.8	524	17	CNS01UYO
17	67	14.7	662	12	BG592447
18	67	14.7	740	17	BQ504880
19	66.4	14.6	1101	17	CNS00D77
20	66.2	14.5	795	17	BH460882
21	66.2	14.5	814	17	BH695520
22	66.2	14.5	1001	17	CNS0155H
23	66	14.5	945	17	CNS04DQK
24	66	14.5	945	17	CNS00Z2U
25	65.8	14.4	843	17	CNS00CS1
26	65.4	14.4	769	17	CNS005XX
27	65.2	14.3	660	17	BH183498
28	65.2	14.3	660	17	CNS070M7
29	65	14.3	876	17	CNS009G1
30	65	14.3	1101	17	CNS00EVL
31	64.6	14.2	1101	17	CNS016L1
32	64.2	14.1	1092	17	CNS020K7
33	64.2	14.1	1101	17	CNS004EW
34	64.2	14.1	1101	17	CNS003BD
35	63.8	14.0	752	17	BH693739
36	63.8	14.0	843	17	CNS00CS1
37	63.8	14.0	883	17	AZ550845
38	63.8	14.0	1184	17	CNS04P4P
39	63.6	13.9	1027	17	CNS02T50
40	63.6	13.9	1101	17	CNS001PB
41	63.6	13.9	1101	17	CNS00YWL
42	63.6	13.9	1200	17	CNS016CO
43	63.4	13.9	975	17	BH179465
44	63.4	13.9	1101	17	CNS00E07
45	63.4	13.9	1201	17	CNS015Z2

ALIGNMENTS

RESULT 1  
CNS00FYG 1101 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence TRF3 end of BAC:  
DEFINITION BACR32N04 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL071206.1 GI:4951245  
VERSION AL071206  
KEYWORDS Drosophila melanogaster.  
SOURCE Drosophila melanogaster.  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrozoa; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1101)  
AUTHORS GSS.  
TITLE Submitted (02-JUN-1999) - FRANCE (E-mail : segre@genoscope.cns.fr  
JOURNAL Direct Submission  
Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : segre@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseogawa and Aaron Mammasser in Pieter de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

Result No.	Score	Query Match	Length	DB ID	Description
1	75.2	16.5	1101	17	CNS00FYG
2	74.8	16.4	905	17	CNS00KHX
3	73.2	16.1	928	17	CNS00DKY
4	72.6	15.9	976	17	CNS04ESM
5	72.6	15.9	1101	17	CNS00EVL
6	72.6	15.9	1225	17	CNS0161D

LOCATION: 832, 833, 838, 842, 847, 849, 850, 853, 856, 857  
OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-7035

Query Match 12.8%; Score 58.2; DB 9; Length 858;  
Best Local Similarity 41.9%; Pred. No. 0.23;  
Matches 144; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

OY 53 TGTGCTTGCATATTAAGATGACTGTAATAGCTTAAATGATAATAAGCATATAGA 112  
DB 419 TTTGGTTTNTTAAATAAANNNTGANAANNTNCCCTATNNNTTGAAAAAATANAAA 360  
OY 113 TTTTGAATATAGTATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTC 172  
DB 359 AAAATTTTNGNGAAATTTAAAAAATTTTNNAAAAGNNNNCAAAAATTAANNNTTTT 300  
OY 173 CAAGCCCATGAAAATTTAATGCTTTAATTAATTAATTAATTAATTAATTTTCAT 232  
DB 299 TNGTTNAAAAAANANNTNTTTAATTTTAAGNTTTTANANANNTTTTNN 240  
OY 233 ATGTAAATTTAATGCGATATAGTGGATTTTCAATTTATTTTAAAAAATAAAAA 292  
DB 239 ANNNTAAATTTTNTTAAANANTAAANNCTTTTTTTTTTTTTTTAAANNNNNA 180  
OY 293 CTTACCCATATTAATGCGTAACATTAATTAATTAATTAATTAATTAATTAATTC 352  
DB 179 AA 120  
OY 353 AACCTAAATAATCGGTGCGGAGCGGTTCGATCGGTTTAGTTC 396  
DB 119 AAAAAAAAAAGTACTCGGCCGCCACCGCTAAGCGGAAATTC 76

RESULT 2  
US-10-224-562-3  
Sequence 3, Application US/10224562  
Publication No. US200300222929A1  
GENERAL INFORMATION:  
APPLICANT: YAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: C1001098DIY  
CURRENT APPLICATION NUMBER: US/10/224-562  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 53332  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-224-562-3

Query Match 12.5%; Score 57; DB 9; Length 53332;  
Best Local Similarity 49.8%; Pred. No. 1.2;  
Matches 144; Conservative 0; Mismatches 145; Indels 0; Gaps 0;  
OY 66 TAAAGATGACTTGAATAATAGCTTAAATTAATTAATTAATTAATTAATTAATAG 125  
DB 31283 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 31342  
OY 126 TATTTTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 185  
DB 31343 ATTTTAT 31402  
OY 186 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 245  
DB 31403 ATTTTAT 31462  
OY 246 TCGGTATGATGAT 305  
DB 31463 TTTTAT 31522

OY 306 TCGGTACGATTAATGATTTATTAATAAATCTAGCGTCTTCCAGGAAGAA 354  
DB 31523 TAT 31571

RESULT 3  
US-09-801-861-3  
Sequence 3, Application US/09801861  
Patent No. US20020119544A1  
GENERAL INFORMATION:  
APPLICANT: YAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: C1001098  
CURRENT APPLICATION NUMBER: US/09/801,861  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 53332  
TYPE: DNA  
ORGANISM: Human  
US-09-801-861-3

Query Match 12.5%; Score 57; DB 10; Length 53332;  
Best Local Similarity 49.8%; Pred. No. 1.2;  
Matches 144; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

OY 66 TAAAGATGACTTGAATAATAGCTTAAATTAATTAATTAATTAATTAATTAATAG 125  
DB 31283 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 31342  
OY 126 TATTTTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 185  
DB 31343 ATTTTAT 31402  
OY 186 AAATTTAATGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 245  
DB 31403 ATTTGAT 31462  
OY 246 TCGGTATGATGAT 305  
DB 31463 TTTTAT 31522  
OY 306 TCGGTACGATTAATGATTTATTAATAAATCTAGCGTCTTCCAGGAAGAA 354  
DB 31523 TAT 31571

RESULT 4  
US-10-239-676-151/C  
Sequence 151, Application US/10239676  
Publication No. US20030082609A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation  
FILE REFERENCE: 5013.1003  
CURRENT APPLICATION NUMBER: US/10/239,676  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 10019173.8  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-239-676-151/C

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCR-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/buffalo.edu/bac.htm.

FEATURES source Location/Qualifiers

1..928 /organism="Drosophila melanogaster" /db\_xref="taxon:7227" /clone\_1fb="RPCR-98" /note="end : 17"

BASE COUNT 262 a 70 c 84 g 321 t 191 others

Query Match 16.1%; Score 73.2; DB 17; Length 928; Best Local Similarity 32.7%; Pred. No. 0.0023; Matches 98; Conservative 81; Mismatches 121; Indels 0; Gaps 0;

64 AATAAAGACTGCTGAAATAGCTTAAATATATATAAATGATATTTAGGAAAT 123
871 AA 812
124 AGTATTTGAGTTTAACTTACTTACTGCTTGAACAGTTTTTATAATCCAGGCCATG 183
811 WTTT 752
184 AAAAAATTTAAATGCTTTTAACTTACTTAAATTTTTCATATGTAATAATTT 243
751 WAAAAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 692
244 AATCGGTACTGCTGAAATAGCTTAAATATATATAAATGATATTTAGGAAAT 303
691 WTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 632
304 TATCGGTACTGCTGAAATAGCTTAAATATATATAAATGATATTTTAAATTTTAAATTT 363
631 AATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 572

RESULT 4 CINS04E5M 976 bp DNA linear GSS 21-MAY-2000
LOCUS CINS04E5M Tetradodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 103P02 of library G from Tetradodon nigroviridis, genomic survey
sequence.
ACCESSION AL286627.1 GI:8025084
VERSION GSS; genome survey sequence.
KEYWORDS Tetradodon nigroviridis.
SOURCE Tetradodon nigroviridis.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
Tetraodontidae; Tetradodon.

REFERENCE 1 (bases 1 to 976)
AUTHORS Roest-Crolius,H., Jallion,O., Dasliya,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Wesselsbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetradodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 976)
AUTHORS Roest-Crolius,H., Jallion,O., Dasliya,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Wesselsbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater puterfish Tetradodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 976)

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-Apr-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradodon.
FEATURES source Location/Qualifiers

1..976 /organism="Tetradodon nigroviridis" /db\_xref="taxon:998837" /clone\_1fb="G" /clone\_1fb="G" /note="Genoscope sequence ID : COB6103DH01Lp1-end : T7"

BASE COUNT 243 a 151 c 137 g 327 t 118 others

Query Match 15.9%; Score 72.6; DB 17; Length 976; Best Local Similarity 41.1%; Pred. No. 0.0028; Matches 123; Conservative 52; Mismatches 117; Indels 7; Gaps 1;

3 AAACATATTCATACATTTGCTTGCATCATATATGCTGAAATAGCTTGGCCCTGC 62
624 MAMMMNNWDAA 683
63 TAATAAAGATTAAGTAAATAGCTTAAATATATATAAATGATATTTAGGAAAT 122
684 TTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 743
123 TAGTATTTGAGTTTAACTTACTTACTGCTTGAACAGTTTTTATAATCCAGGCCATG 175
744 WAAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 803
176 GGCCCATGAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 235
804 AATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 863
236 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 294
864 TWWTWTNTTANAAMWATATAATATATATATATATATATATATATATATATATATAT 922

RESULT 5 CINS00EVL/C 1101 bp DNA linear GSS 04-JUN-1999
LOCUS CINS00EVL/C Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29823 of RPCR-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL0659706 GI:4949849
VERSION GSS.
KEYWORDS Drosophila melanogaster.
SOURCE Drosophila melanogaster.
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Drosophila melanogaster.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Osoegawa and
Aaron Memmeser in Pletier de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCR-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's



Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

```

FEATURES
  source
    Location/Qualifiers
      1..928
      /organism="Drosophila melanogaster"
      /db_xref="taxon:7227"
      /clone="BACR27A24"
      /plasmid="RPCI-98"
      /note="end : 977"
BASE COUNT 262 a 70 c 84 g 321 t 191 others
ORIGIN

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Query Match 15.8%; Score 72; DB 17; Length 928;  
 Best Local Similarity 31.1%; Pred. No. 0.0036;  
 Matches 117; Conservative 93; Mismatches 166; Indels 0; Gaps 0;

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OY 60 TGCATAAATAAAGTAAGTTAAAGCTTAGTAAATAATGATATGATTGATAGG 119
  |||:||||| | :|:| | : | :|:| | | | | | | | | | | | | | |
DB 500 TGTATATAATTTTATKAWMAAAWAAATTTTWMWAAAAAATTTTATTTTWT 559
OY 120 AATTAGCTTTGTTAGTTAATTACTTTAGCTTTAATAGCTTTTATAATTCCAGGCC 179
  |||:||||| | :|:| | : | :|:| | | | | | | | | | | | | | |
DB 560 TTTTATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 619
OY 180 CATGAAATTTAAAGTTATAGTTAATTAACTATATAATTTTCTATATATATAA 239
  |||:||||| | :|:| | : | :|:| | | | | | | | | | | | | | |
DB 630 AATAATATATAATAATATTTTATTAATTTAATAAATAAATAAATAAATAAATAA 679
OY 240 AATTAAATCGTATGATTTTAAATTTTCAATTTTATTAATAAATAAATAAATAA 299
  |||:||||| | :|:~| | : | :|:| | | | | | | | | | | | | | |
DB 680 AAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 739
OY 300 TAAATATCGGATGATTTAGTTAATAAATAAATAAATAAATAAATAAATAAATAA 359
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 740 TMMWMAATTTTWDGNMNNNNAAMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM 799
OY 360 AAATCGTTCGTCGCGGAGGCTTCGATCGTTCGATTTTCAAAATTCATTTGACAC 419
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 800 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 479
OY 420 TCCTAGTTGTGTAT 435
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 860 WTTTTTTTTTTTTTTTTT 875
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |

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RESULT 8  
 CENS014P0 987 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC  
 DEFINITION BACN1222 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL104456.1 GI:5616067  
 VERSION AL104456  
 KEYWORDS  
 SOURCE Drosophila melanogaster.  
 ORGANISM Drosophila melanogaster.  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Braconyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE  
 AUTHORS Direct Submission  
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage; BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP).

<http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelosBAC11.

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FEATURES
  source
    Location/Qualifiers
      1..987
      /organism="Drosophila melanogaster"
      /db_xref="taxon:7227"
      /clone="BACN12P22"
      /plasmid="DrosBAC"
      /plasmid="pBelosBAC11"
      /note="end : SP6"
BASE COUNT 257 a 122 c 122 g 241 t 245 others
ORIGIN

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Query Match 15.8%; Score 72; DB 17; Length 987;  
 Best Local Similarity 31.7%; Pred. No. 0.0035;  
 Matches 114; Conservative 88; Mismatches 158; Indels 0; Gaps 0;

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OY 3 AAACATATTCAATTCATTTGCTTACCTCATTAATGCTTGAATFACCTTCCCTCC 62
  |||:||||| | :|:| | : | :|:| | | | | | | | | | | | | | |
DB 578 AADRARRRRRRRRRBRKRKRKRKRKRKRKRKRKRKRKRKRKRKRKRKRKRKRKR 637
OY 63 TATAAAGTACTTGAATTAATGCTTGAATTAATTAATGATTAATGATTTAGGANT 122
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 638 AMMAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 697
OY 123 TAGTATTTTGTAGTTAATTACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 182
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 698 NNNMTTWMTTMMWMTTMMWMTTMMWMTTMMWMTTMMWMTTMMWMTTMMWMTTMM 757
OY 183 GAAAATAATAAGCTTTTAACTTTAAATTAATAAATTTTCTATGATAAATTT 242
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 758 AAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 817
OY 243 TAAATATCGGATGATTTAGTTAATAAATAAATAAATAAATAAATAAATAAATAA 302
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 818 TAAATATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 877
OY 303 TTAATCGGATGATTTAGTTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 362
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |
DB 878 WAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 937
  |||:||||| | :|:~| | : | :|:~| | | | | | | | | | | | | | | |

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RESULT 9  
 CENS00LT2 1101 bp DNA linear GSS 14-JUN-1999  
 LOCUS Drosophila melanogaster genome survey sequence T673 end of BAC  
 DEFINITION BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL078714  
 VERSION AL078714.1 GI:5102004  
 KEYWORDS  
 SOURCE Drosophila melanogaster.  
 ORGANISM Drosophila melanogaster.  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Braconyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE  
 AUTHORS Direct Submission  
 JOURNAL Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage; BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of

APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT221C1  
CURRENT APPLICATION NUMBER: US/10/074.045  
CURRENT FILING DATE: 2002-02-14  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 60  
LENGTH: 3991  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-074-045-60

Query Match 11.5% Score 52.6; DB 9; Length 3991;  
Best Local Similarity 52.0%; Pred. No. 3.3;  
Matches 143; Conservative 0; Mismatches 129; Indels 3; Gaps 1;

78 AATAGCTGTTAATAAATGACATTAATGATTTAGGAAATTTAGATTTGAGCTT 137  
1106 AATATATACGCTTAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 3165  
1138 AATAGCTGTTAATAAATGACATTAATGATTTAGGAAATTTAGATTTGAGCTT 197  
1166 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3225  
1198 TATTTAGCTGTTAATAAATGACATTAATGATTTAGGAAATTTAGATTTGAGCTT 257  
1226 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3285  
258 GATATTTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 314  
386 AATATATACGCTTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3345  
315 TTATGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 349  
346 AATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3380

RESULT 13  
US-10-094-240-10  
; Sequence 10, Application US/10094240  
; Publication No. US20030082637A1  
; GENERAL INFORMATION:  
; APPLICANT: ZIEBEL, LAURENCE J.  
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF  
; FILE REFERENCE: N8289  
; CURRENT APPLICATION NUMBER: US/10/094.240  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 10/056,405  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/264,649  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 4985  
; TYPE: DNA  
; ORGANISM: Anopheles gambiae  
US-10-094-240-10

Query Match 11.5% Score 52.4; DB 9; Length 4985;  
Best Local Similarity 49.0%; Pred. No. 3.8;  
Matches 140; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

33 TCATATGCGTAGAATGATTTGCTTGCCTTAATTAATTAATTAATTAATTAATTAATTA 92  
2726 TTATATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2785  
93 AATATATACGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 152  
2786 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2845

153 TGTACAGCTTTTATTAATTCACAGCCCATGAAAAATTTAATGCTTTATGTTTAAAC 212  
2846 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2905  
213 TTACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 272  
2906 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2965  
273 TATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 318  
2966 TTGCTATTTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3011

RESULT 14  
US-10-074-045-60/c  
; Sequence 60, Application US/10074045  
; Publication No. US20030092102A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT221C1  
; CURRENT APPLICATION NUMBER: US/10/074.045  
; CURRENT FILING DATE: 2002-02-14  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 3991  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-074-045-60

Query Match 11.4% Score 52.2; DB 9; Length 3991;  
Best Local Similarity 52.5%; Pred. No. 3.9;  
Matches 137; Conservative 0; Mismatches 123; Indels 1; Gaps 1;

78 AATAGCTGTTAATAAATGACATTAATGATTTAGGAAATTTAGATTTGAGCTT 137  
3355 AATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3296  
138 AATAGCTGTTAATAAATGACATTAATGATTTAGGAAATTTAGATTTGAGCTT 197  
3295 ATTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3236

198 TTATAGCTTTA-ACCTACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 256  
3235 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3176  
257 CGAATTTTTCGAATTTATTTAAATAATTAATTAATTAATTAATTAATTAATTAATTA 316  
3175 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3116  
317 ATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 337  
3115 TTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3095

RESULT 15  
US-09-960-352-5087  
; Sequence 5087, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathiasjan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960.352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 5087

BASE COUNT 277 a 96 c 121 g 382 t 167 others

Query Match 15.2% Score 69.2; DB 17; Length 1043; Best Local Similarity 39.8%; Pred. No. 0.01; Mismatches 135; Indels 0; Gaps 0;

Matches 121; Conservative 48; Mismatches 135; Indels 0; Gaps 0;
OY 59 TTGCTAATTAAGATCTGAAATAGCTTAAATAGCTTAAATAGCAATATAGATTTTACG 118
DB 569 WTATWTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 628
OY 119 GAATTTAGATTTTGGATTTTAACTTATTTGATTTGATTTGATTTGATTTGATTTGATTT 178
DB 629 TMMWTWTTTATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTTW 688
OY 179 CCATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 238
DB 689 TWAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 748
OY 239 AATTTAATCGGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 298
DB 749 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 808
OY 289 CTAATTTATCGGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 358
DB 809 AWAATAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 868
OY 359 AAAA 362
DB 869 AAAA 872

RESULT 12

CNS014PQ/c 987 bp DNA linear GSS 26-JUL-1999
LOCUS CNS014PQ Drosophila melanogaster genome survey sequence Sp6 end of BAC
DEFINITION BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL104456.1 GI:5616067
VERSION AL104456
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 987)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES source
Location/Qualifiers
1..987
/organism="Drosophila melanogaster"
/db\_xref="taxon:7227"
/clone\_lib="BACN12P22"
/clone="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"

BASE COUNT 257 a 122 c 122 g 241 t 245 others

Query Match 15.0% Score 68.4; DB 17; Length 987; Best Local Similarity 30.3%; Pred. No. 0.014; Mismatches 161; Indels 4; Gaps 1;

Matches 117; Conservative 104; Mismatches 161; Indels 4; Gaps 1;
OY 63 TAAATAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 122
DB 951 MWWWMMWWTT 892
OY 123 TAGTATTTTGGATTTTAACTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 182
DB 891 WMATWTTTATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTW 832
OY 183 GAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCAATGTA 238
DB 831 MFTNRMMWMTTATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTW 772
OY 239 AATTTAATCGGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 298
DB 771 AATTTAATTAATTTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 712
OY 289 CTAATTTATCGGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 358
DB 711 WAWWWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAA 652
OY 359 AAAATCGGTGCGGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 418
DB 651 WTKWTK 592
OY 419 CTCCTAGTTGTTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 444
DB 591 YYYYYHYHTTHTTHTTCTTAAWHH 566

RESULT 13

CNS015WU 1203 bp DNA linear GSS 26-JUL-1999
LOCUS CNS015WU Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN15F10 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL106008.1 GI:5619558
VERSION AL106008
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1203)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES source
Location/Qualifiers
1..1203
/organism="Drosophila melanogaster"
/db\_xref="taxon:7227"
/clone\_lib="BACN15F10"
/clone="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"
BASE COUNT 288 a 103 c 235 g 253 t 324 others

ORIGIN

Query Match 15.0%; Score 68.4; DB 17; Length 1203; Best Local Similarity 37.3%; Pred. No. 0.013; Mismatches 100; Conservative 58; PindMatches 110; Indels 0; Gaps 0;

67 AAGATGCTGAAATAGCTTAAATTAATAGCATATGATTTTGGAAATAGT 126
63 AAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 995
127 ATTTGGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 186
996 WTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1055
187 AATTAATGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 246
1056 AATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1115
247 CGTATGCTGAAATAGCTTAAATTAATTAATTAATTAATTAATTAAT 306
1116 AATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1175
307 CGTATGCTGAAATAGCTTAAATTAATTAATTAATTAATTAATTAAT 334
1176 AATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1203

RESULT 14

CNS00E07 1101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence TE3 end of BAC:
BACR23901 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL069440.1 GI:4949583
GSS:
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydrozoidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequence:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefgenoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2: cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/db\_xref="taxon:7227"
/clone="BACR23901"
/clone.lib="RPCI-98"
/note="end: TE3"

BASE COUNT 366 a 66 c 104 g 351 t 214 others
ORIGIN Query Match 15.0%; Score 68.2; DB 17; Length 1101;

Best Local Similarity 38.3%; Pred. No. 0.015; Mismatches 128; Conservative 53; Mismatches 153; Indels 0; Gaps 0;

3 AACATATTCATCATGTTGTTGCTACACATATGCTAGAAATGCTGCTGC 62
855 AATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 796
63 TAATAAAGATGCTGAAATAGCTTAAATTAATTAATTAATTAATTAATTA 122
795 TATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 736
123 TAGTATTTGAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 182
735 TTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 676
183 GAAATAATTAATGCTTAAATTAATTAATTAATTAATTAATTAATTAAT 242
675 AATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 616
243 TAATCGTATGCTGAAATAGCTTAAATTAATTAATTAATTAATTAATTA 302
615 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 556
303 TTAATCGTATGCTGAAATAGCTTAAATTAATTAATTAATTAATTAAT 336
555 AATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 522

RESULT 15

CNS001FB/C 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TE3 end of BAC:
BACR04A23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL060732.1 GI:4939397
GSS:
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydrozoidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequence:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefgenoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2: cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/db\_xref="taxon:7227"
/clone="BACR04A23"
/clone.lib="RPCI-98"
/note="end: TE3"

BASE COUNT 288 a 110 c 103 g 491 t 109 others
ORIGIN Query Match 15.0%; Score 68.2; DB 17; Length 1101;

Query Match 14.9%; Score 68; DB 17; Length 1101;  
 Best Local Similarity 37.8%; Pred. No. 0.016;  
 Matches 125; Conservative 52; Mismatches 154; Indels 0; Gaps 0;

QY	3	AAACGATTC	CAATC	ATGCTG	CTACTC	CTCAAT	TCGC	TAAT	TCG	GAAT	CTT	GTGC	CTGC	62		
DB	996	AAAAAAAAA	TTWATA	TATTT	NTNAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	937		
QY	63	TAATAAG	ACTTGA	AAAGCT	TACTT	AAAAT	ATATAA	TATAG	CTT	TAG	GAAT	122				
DB	936	AAAAAT	TAATA	TAAAT	AAAT	AAAT	AAAT	AAAT	AAAT	AAAT	AAAT	AAAT	AAAT	877		
QY	123	TAGTAT	TTGAG	TTAAT	TACT	TAT	TACT	TGA	CAG	TTT	TAT	TAT	TCC	AGCCCAT	182	
DB	876	AAWAAAA	AAATW	AAAAA	AAATW	AAAAA	AAATW	AAAAA	AAATW	AAAAA	AAATW	AAAAA	AAATW	AAAAA	817	
QY	183	GAAAAA	TTTA	AGCT	TAT	TAG	TTT	AACT	TA	CTA	TAT	TA	AAAT	TTT	242	
DB	816	TTTTAAT	TATAT	TATTA	TAAAT	WTWAAAA	AAAAA	TAAW	AAATW	TAAW	AAATW	AAAAA	AAAAA	757		
QY	243	TAATCG	TATAG	TTCG	ATAT	TTT	TTC	CAAT	TAT	TTT	TAT	AAAA	AAAA	AACT	ACCTAA	302
DB	756	AAAAAT	ATATW	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	697
QY	303	TTATCG	TACAG	TTAT	AGAT	TTAT	ATA	AAAA	333							
DB	696	TAAWAAAA	AAAAAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	666

Search completed: June 9, 2003, 08:01:26  
 Job time : 1132 secs

ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers  
1. .1101

FEATURES  
source /organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="BACR32N04"  
/clone\_11b="RPC1-98"  
/note="end : TET3"  
BASE COUNT 429 a 102 c 128 g 343 t 99 others  
ORIGIN

Query Match 16.5%; Score 75.2; DB 17; Length 1101;  
Best Local Similarity 43.3%; Pred. No. 0.00098;  
Matches 154; Conservative 42; Mismatches 159; Indels 1; Gaps 1;

```
8 TATTCACAACATTTGAGTTGCTCATAAATCGCTAGAACTTTGTCCTTGCCTAATA 67
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
728 TATAAATAAATATATATATATATATATATATATATATATATATATATATATAT 787
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 AAGATACCTGAAATAGCTTAGTTAAATATAATAGCATTAATAGATTAGGAATAGTA 127
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
788 TATAAATAAATATATATATATATATATATATATATATATATATATATATATAT 847
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
128 TTTTACGTTTAACTTATGACTTGTAAAGCTTTTATATATCCCAAGGCCCATGAAA 187
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
848 AATATATATATAAATAATATATATATATATATATATATATATATATATATATAT 907
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
188 ATTTAAAGCTTTTAACTTATATATATATATATATATATATATATATATATATAT 247
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
908 WTTAATATATATATAAATAATATATATATATATATATATATATATATATATATAT 966
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
248 GGTATAGCTGATATTTTTCATATTTTATATATAAATAAATAAATAAATAAATAA 307
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
967 TAAAAATATATATATATATATATATATATATATATATATATATATATATATAT 1026
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
308 GGTACAGTATATATATATATATATATATATATATATATATATATATATATATAT 363
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1027 AAAAAATATATATATATATATATATATATATATATATATATATATATATATAT 1082
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 2  
CNS00KHX/c 905 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:  
DEFINITION BACR17N06 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL077798  
VERSION AL077798.1 GI:4957174  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster.  
ORGANISM Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE Genoscope. Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPC1-98 and was constructed by partial EcorI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers  
1. .905

FEATURES  
source /organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="BACR17N06"  
/clone\_11b="RPC1-98"  
/note="end : T7"  
BASE COUNT 388 a 82 c 77 g 194 t 164 others  
ORIGIN

Query Match 16.4%; Score 74.8; DB 17; Length 905;  
Best Local Similarity 37.8%; Pred. No. 0.0012;  
Matches 130; Conservative 62; Mismatches 152; Indels 0; Gaps 0;

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19 TTGTAGTTGCTACCTAATATAGCAATAGTCTTGTGCTTGCCTAATAAATGACTGTA 78
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
852 TTTTWTATATATATATATATATATATATATATATATATATATATATATATATAT 793
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
79 AATAGCTTAGTTAAATATATAATAGCAATATAGATTTTGAATAGTATTTGAGTTTA 138
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
792 ATATWTATATATATATATATATATATATATATATATATATATATATATATAT 733
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
139 ATTACTTATGACTTGTAAAGCTTTTATATATCCCAAGGCCCAAGAAAATTTAATGCTT 198
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
732 TAAAAAAMWTAATATATATATATATATATATATATATATATATATATATATAT 673
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199 TATTTAGTTTAACTTATATATATATATATATATATATATATATATATATATAT 258
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
672 TTTTAAAMWTAATATATATATATATATATATATATATATATATATATATATAT 613
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
259 ATATTTTCAATATATATATATATATATATATATATATATATATATATATATAT 318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
612 TTATWTATATATATATATATATATATATATATATATATATATATATATATAT 553
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
319 AGATTTATATATATATATATATATATATATATATATATATATATATATATAT 362
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
552 MAMHWAAMWTAATATATATATATATATATATATATATATATATATATATATAT 509
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 3  
CNS00DKY/c 928 bp DNA linear GSS 04-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #  
DEFINITION BACR27A24 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL071865  
VERSION AL071865.1 GI:4948170  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster.  
ORGANISM Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE Genoscope. Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of

P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES
source
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db\_xref="taxon:7227"
/clone="BACR29B23"
/clone\_1lb="RP01-98"
/clone\_1lb="RP01-98"
/note="end : T7"
BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN
Query Match 15.9% Score 72.6; DB 17; Length 1101;
Best Local Similarity 35.1%; Pred. No. 0.0027;
Matches 150; Conservative 74; Mismatches 203; Indels 0; Gaps 0;

http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES
source
Location/Qualifiers
1..1225
/organism="Drosophila melanogaster"
/db\_xref="taxon:7227"
/clone="BACR29B23"
/clone\_1lb="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
BASE COUNT 266 a 128 c 38 g 368 t 425 others
ORIGIN
Query Match 15.9% Score 72.6; DB 17; Length 1225;
Best Local Similarity 37.4%; Pred. No. 0.0026;
Matches 114; Conservative 61; Mismatches 130; Indels 0; Gaps 0;

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -

